

GenCore version 5.1.4\_p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: March 3, 2003, 21:30:10 ; Search time 4788 Seconds  
(without alignments)  
10606.599 Million cell updates/sec

Title: US-10-017-621-3

Perfect score: 1745

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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2	22.8	1.3	50	6 A93721	A93721 Sequence 8
3	22.4	1.3	50	6 A93722	A93722 Sequence 9
4	22.2	1.3	47	6 I84671	I84671 Sequence 5
5	22	1.3	50	6 AX159452	AX159452 Sequence 5
6	21.6	1.2	31	6 AX246673	AX246673 Sequence
7	21.4	1.2	42	6 AX182243	AX182243 Sequence
8	21.4	1.2	42	6 AX382049	AX382049 Sequence
9	21.4	1.2	46	6 AR032544	AR032544 Sequence
10	21.4	1.2	46	6 AR0209208	AR0209208 Sequence 15
11	21.4	1.2	46	6 I29284	I29284 Sequence 15
12	21.4	1.2	46	6 I90958	I90958 Sequence 15
13	21	1.2	31	6 AX248015	AX248015 Sequence
14	21	1.2	46	6 AX186238	AX186238 Sequence
15	20.8	1.2	46	6 A98791	A98791 Sequence 24
16	20.6	1.2	21	6 AX153958	AX153958 Sequence
17	20.6	1.2	45	6 AR022074	AR022074 Sequence
18	20.6	1.2	45	6 I55009	I55009 Sequence 33
19	20.6	1.2	45	6 I92864	I92864 Sequence 38
20	20.4	1.2	48	6 AR079723	AR079723 Sequence
21	20.4	1.2	48	6 AR081253	AR081253 Sequence
22	20.4	1.2	48	6 AR170613	AR170613 Sequence
23	20.2	1.2	40	6 AR200128	AR200128 Sequence
24	20.2	1.2	40	6 I68030	I68030 Sequence 13
25	20.2	1.2	45	6 AX225269	AX225269 Sequence
26	20.2	1.2	49	6 AR083818	AR083818 Sequence
27	20.2	1.2	49	9 S82032	S82032 Wtl-Hila,
28	20.2	1.2	50	6 AX233404	AX233404 Sequence
29	20	1.1	36	6 A07324	A07324 Synthetic D
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31	20	1.1	41	6 BD007098	BD007098 Targeted
32	20	1.1	44	6 A07325	A07325 Synthetic D
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34	20	1.1	46	6 E52011	E52011 IL-6 recept
35	19.8	1.1	46	6 AX036348	AX036348 Sequence
36	19.8	1.1	46	6 AX036350	AX036350 Sequence
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38	19.8	1.1	48	23 BD004595	BD004595 Vitamin D
39	19.6	1.1	39	6 AX452342	AX452342 Sequence
40	19.6	1.1	42	6 AR153233	AR153233 Sequence
41	19.6	1.1	45	6 I17261	I17261 Sequence 27
42	19.6	1.1	45	6 I47720	I47720 Sequence 19
43	19.6	1.1	50	6 AR032970	AR032970 Sequence
44	19.6	1.1	50	6 AR209634	AR209634 Sequence
45	19.6	1.1	50	6 AX199648	AX199648 Sequence

# ALIGNMENTS

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LOCUS H. sapiens mRNA for Cdk activating kinase.  
DEFINITION X76171  
ACCESSION X76171.1 GI:429096  
VERSION X76171.1  
KEYWORDS activating kinase; protein kinase.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 49)  
AUTHORS Hall, F. L.  
TITLE Direct Submission  
JOURNAL Submitted (08-NOV-1993) F. L. Hall, Childrens Hospital Los Angeles,

Pred. No. is the number of results predicted by chance to have a

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Division of Orthopaedic Surgery, 4650 Sunset Boulevard, Los
Angeles, CA, 90027, USA
2 (bases 1 to 49), USA
Wu, L. and Hall, F.L.
Unpublished
3 (bases 1 to 49)
Wu, L., Yee, A., Liu, L., Carbonaro Hall, D., Venkatesan, N., Tolo, V.T.
and Hall, F.L.
TITLE
Molecular cloning of the human CAK1 gene encoding a
cyclin-dependent kinase-activating kinase
JOURNAL
Oncogene 9 (7), 2089-2096 (1994)
MEDLINE
94268852
PUBMED
8208556
FEATURES
source
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/db_xref="taxon:9606"
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LOCUS
DEFINITION Sequence 8 from Patent W09732891.
ACCESSION A93721
VERSION A93721.1 GI:6741893
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 50)
AUTHORS Rose-John, S.
TITLE CONJUGATE FOR MODIFYING INTERACTIONS BETWEEN PROTEINS
JOURNAL Patent: WO 9732891-A 8 12-SEP-1997;
AN ANTE GENTECHNOLOGIE SYST (DE); ROSE JOHN STEFAN (DE)
FEATURES
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Location/Qualifiers
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Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
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ACCESSION A93722
VERSION A93722.1 GI:6741894
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 50)
AUTHORS Rose-John, S.
TITLE CONJUGATE FOR MODIFYING INTERACTIONS BETWEEN PROTEINS
JOURNAL Patent: WO 9732891-A 9 12-SEP-1997;
AN GENAMNTE GENTECHNOLOGIE SYST (DE); ROSE JOHN STEFAN (DE)
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Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
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I84671
LOCUS
DEFINITION Sequence 5 from patent US 5696086.
ACCESSION I84671
VERSION I84671.1 GI:3022191
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 47)
AUTHORS Avraham, H. Karsenty, and Godowski, P. J.
TITLE Methods and kits using macrophage stimulating protein
JOURNAL Patent: US 5696086-A 5 09-DEC-1997;
AN ANTE GENTECHNOLOGIE SYST (DE); ROSE JOHN STEFAN (DE)
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Location/Qualifiers
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Matches 30; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
Qy 241 GCGGGAGTGCCTCGAGAGAGGCCCCACACAGCTGCTGCTCTG 283
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Db 2 GGACGAATCCACCATGGGTGGCTGCCACCTCCCTGCTGCTCTG 44

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LOCUS
DEFINITION Sequence 2780 from Patent W00140521.
ACCESSION AXI59452
VERSION AXI59452.1 GI:14540783
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;

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REFERENCE 1 (bases 1 to 50)  
 AUTHORS Shimketa, R.A. and Leach, M.  
 TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof  
 JOURNAL Patent: WO 0140521-A 2780 07-JUN-2001;  
 Curagen Corporation (US)  
 FEATURES Location/Qualifiers  
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 Accession number c942160243"  
 misc\_feature 26  
 /note="2 of 2 allelic variants (2779 is other entry)"  
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 Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
 QY 1642 CGCTGAGGATGACACACCCCTACAGGGCAGCC 1679  
 Db 11 CTGCTGAGCCCTGACACACCCCTCTGCTGGCCGCC 48

RESULT 6  
 AX248673  
 LOCUS AX248673 31 bp DNA linear PAT 28-SEP-2001  
 DEFINITION Sequence 752 from Patent WO0166800.  
 ACCESSION AX248673  
 VERSION AX248673.1 GI:15863296  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 31)  
 AUTHORS Cargill, M., Ireland, J.S. and Lander, E.S.  
 TITLE Human single nucleotide polymorphisms  
 JOURNAL Patent: WO 0166800-A 752 13-SEP-2001;  
 WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)  
 FEATURES Location/Qualifiers  
 source 1..31  
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 LOCUS AX182243 42 bp DNA linear PAT 06-AUG-2001  
 DEFINITION Sequence 53 from Patent WO0142441.  
 ACCESSION AX182243  
 VERSION AX182243.1 GI:15133518  
 KEYWORDS  
 SOURCE synthetic construct.  
 ORGANISM synthetic construct.  
 artificial sequences.  
 REFERENCE 1 (bases 1 to 42)  
 AUTHORS Reddy, S.I., Sadhu, L.I., Shukla, V.C. and Ferralolo, G.I.  
 TITLE plasmid transformation

JOURNAL Patent: WO 0142441-A 53 14-JUN-2001;  
 International Centre for Genetic Engineering and Biotechnology (IT)  
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 /db\_xref="taxon:32630"  
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 Db 35 ACCTAGGGTCTCTGGCGACCTTCGATCTGCA 5

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 DEFINITION Sequence 53 from Patent WO0206497.  
 ACCESSION AX382049  
 VERSION AX382049.1 GI:19576871  
 KEYWORDS  
 SOURCE synthetic construct.  
 ORGANISM synthetic construct.  
 artificial sequences.  
 REFERENCE 1  
 AUTHORS Reddy, V.S. and Sadhu, L.  
 TITLE Transplasmatic plants  
 JOURNAL Patent: WO 0206497-A 53 24-JAN-2002;  
 International Centre for Genetic Engineering and Biotechnology (IT)  
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 Db 35 ACCTAGGGTCTCTGGCGACCTTCGATCTGCA 5

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 AR032544  
 LOCUS AR032544 46 bp DNA linear PAT 29-SEP-1999  
 DEFINITION Sequence 156 from patent US 5869241.  
 ACCESSION AR032544  
 VERSION AR032544.1 GI:5948149  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 46)  
 AUTHORS Edwards, C.A., Cantor, C.R., Andrews, B.M., Turin, L.M. and Fry, K.E.  
 TITLE Method of determining DNA sequence preference of a DNA-binding molecule

JOURNAL Patent: US 5869241-A 156 09-FEB-1999;  
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AR209208 LOCUS AR209208 DNA linear PAT 20-JUN-2002					
DEFINITION Sequence 156 from patent US 6384208.					
ACCESSION AR209208					
VERSION AR209208.1 GI:21510563					
KEYWORDS unknown.					
SOURCE /organism='unknown'					
ORGANISM Unknown; 9 a 14 c 16 g 7 t					
REFERENCE Unclassified.					
AUTHORS 1 (bases 1 to 46)					
EDWARDS,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.					
TITLE Sequence directed DNA binding molecules compositions and methods					
JOURNAL Patent: US 6384208-A 156 07-MAY-2002;					
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I29284 LOCUS I29284 DNA linear PAT 06-FEB-1997					
DEFINITION Sequence 156 from patent US 5578444.					
ACCESSION I29284					
VERSION I29284.1 GI:1820075					
KEYWORDS unknown.					
SOURCE /organism='unknown'					
ORGANISM Unknown; 9 a 14 c 16 g 7 t					
REFERENCE Unclassified.					
AUTHORS 1 (bases 1 to 46)					
EDWARDS,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.					
TITLE Sequence-directed DNA-binding molecules compositions and methods					
JOURNAL Patent: US 5578444-A 156 26-NOV-1996;					
FEATURES Location/Qualifiers					
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Dd	2	CGCGTGATTGGACGCTCCACCAATCATCAGGCAGCGCC	40		
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I90958 LOCUS I90958 DNA linear PAT 01-DEC-1998					
DEFINITION Sequence 156 from patent US 5726014.					
ACCESSION I90958					
VERSION I90958.1 GI:3935428					
KEYWORDS					

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OY 550 AAGCCCTCAGCGCGGCTCCGTCGTGTCAGCCTATC 587
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RESULT 15
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ACCESSION A98791
VERSION A98791.1 GI:6781812
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SOURCE     unidentified.
ORGANISM   unidentified.
REFERENCE  1 (bases 1 to 46)
AUTHORS   Hegemann P.
TITLE     METHOD FOR PRODUCING NUCLEIC ACID POLYMERS
JOURNAL   Patent: WO 9910358-A 24 04-MAR-1999;
          HEGEMANN PETER (DE)
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OY 500 TGCGTCAGCGGCTACTCGGAGAGCGTGACCTC 531
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DB 37 TGCCGAGCGGCTACTCGGAGGAGCGGACCATC 6

Search completed: March 4, 2003, 00:06:28
Job time : 4794 secs

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GenCore version 5.1.4.p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: March 3, 2003, 22:34:05 ; Search time 2628 Seconds  
(without alignments)  
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Title: US-10-017-621-3

Perfect score: 1745

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Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

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21: em\_gss\_vrt:\*

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23: em\_gss\_mam:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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6	21	1.2	50	9	AU102877

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C	8	21	1.2	50	13	BM397711
	9	20.8	1.2	46	17	A2993993
	10	20.6	1.2	48	17	A2311362
C	11	20.6	1.2	50	9	AU106960
C	12	20.4	1.2	47	17	A2311536
C	13	20.2	1.2	45	17	A2985975
C	14	20.2	1.2	49	9	A204601
C	15	20	1.1	40	9	A1475974
	16	20	1.1	50	17	BH811451
	17	19.8	1.1	49	14	W39000
C	18	19.4	1.1	50	9	AU104829
	19	19.2	1.1	44	12	BG422154
	20	19.2	1.1	49	17	A2450961
C	21	19.2	1.1	50	9	AU103357
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C	23	19.2	1.1	50	9	AU103359
C	24	19.2	1.1	50	9	AU103361
	25	19.2	1.1	50	9	AU103381
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	27	19.2	1.1	50	9	AU106349
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	31	19	1.1	50	9	AU107320
C	32	18.8	1.1	34	9	AA972479
C	33	18.8	1.1	43	17	BH857724
	34	18.8	1.1	46	17	BH790015
	35	18.8	1.1	50	9	AU102939
	36	18.8	1.1	50	9	AU103583
C	37	18.8	1.1	50	9	AU104587
C	38	18.8	1.1	50	9	AU105918
C	39	18.6	1.1	44	17	TA165G050
C	40	18.6	1.1	45	9	A1250043
	41	18.6	1.1	49	17	A2966392
	42	18.6	1.1	50	9	AU103382
	43	18.6	1.1	50	9	AU103553
C	44	18.6	1.1	50	9	AU104162
C	45	18.6	1.1	50	13	BT910989

## ALIGNMENTS

RESULT 1  
N78054  
LOCUS  
DEFINITION  
Yv71905.r1 Soares fetal liver spleen INFLS Homo sapiens CDNA clone  
IMAGE:248216 5' similar to gb:X66363 SERINE/THREONINE-PROTEIN  
KINASE PCTAIRE-1 (HUMAN);, mRNA sequence.

ACCESSION  
N78054  
VERSION  
N78054.1 GI:1240755  
KEYWORDS  
EST.  
SOURCE  
human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 46)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.P., Chiapelli, B.,

Chillore, S., Dietrich, N., DuBoque, T., Favell, A., Gish, W., Hawkins

, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore

, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Moore

Schellenberg, K., Soares, M.B., Tan, F., Thierry-Neg, J., Trevisan, E.,

Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.

Generation and analysis of 280,000 human expressed sequence tags

Genome Res. 6 (9), 807-828 (1996)

97044478

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu



BASE COUNT	11 a	14 c	17 g	17 g	6 t

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Matches 28; Conservative 0; Mismatches 8
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[illegible]

**AU107934**

HSI01159, mRNA sequence:

**СУБМАРИНЫ  
МОСКВА**

304000

## REFERENCE

**TITLE**

**JOURNAL**

**COMMENT**

**0**

**SOUR**

## ORIGIN

## Query M

March 20

337  
03

• 1

## RESULT 5

## Locals



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ACCESSION   AU102877
VERSION     AU102877.1  GI:13552398
KEYWORDS    EST.
SOURCE      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 50)
AUTHORS     Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
            , H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
            , Y., Nakamura, Y., Suyama, A. and Sugano, S.
TITLE       Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
JOURNAL     EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE     21270072
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: yusuzuki@ims.u-tokyo.ac.jp
            Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
            , S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="COL3073"
                     /clone_lib="Sugano Homo sapiens cDNA library"
                     /note="Differential display comparison of untreated and
                     dimethylformate treated U937 cells"
BASE COUNT          11 a 20 c 10 g
ORIGIN
Query Match          1.2%; Score 21; DB 9; Length 50;
Best Local Similarity 82.8%; Pred. No. 6.3e+05;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 491 ACATCCGCTGCTGAGGCTACCTGGAG 519
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Db 1 ACATCCGCTGCTGAGACCTCTGCGAG 29

RESULT 7
AU105237/c
LOCUS         AU105237 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION   HRC08919, mRNA sequence.
ACCESSION   AU105237
VERSION     AU105237.1  GI:13554758
KEYWORDS    EST.
SOURCE      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 50)
AUTHORS     Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
            , H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
            , Y., Nakamura, Y., Suyama, A. and Sugano, S.
TITLE       Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
JOURNAL     EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE     21270072
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: yusuzuki@ims.u-tokyo.ac.jp
            Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
            , S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES             Location/Qualifiers
     source           1..50

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HRC08919"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylformate treated U937 cells"
BASE COUNT          13 a 10 c 22 g 5 t
ORIGIN
Query Match          1.2%; Score 21; DB 9; Length 50;
Best Local Similarity 82.8%; Pred. No. 6.3e+05;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 558 CAGCCGCCCTCGCTGCTGTCAGCCTAT 586
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Db 35 CAGCTCCGCCGCCCATCTCTGCGCCTAT 7

RESULT 8
BM397711/c
LOCUS         BM397711 50 bp mRNA linear EST 17-JAN-2002
DEFINITION   Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM397711
VERSION     BM397711.1  GI:18197764
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila.
            Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE   1 (bases 1 to 50)
AUTHORS     Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel
            , J. and Klobutcher, L.
            EST from Tetrahymena thermophila, strain CU428.1, growing cells
            Unpublished (2002)
            Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source           1..50
                     /organism="Tetrahymena thermophila"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: Bluescript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT          10 a 7 c 23 g 2 t 8 others
ORIGIN
Query Match          1.2%; Score 21; DB 13; Length 50;
Best Local Similarity 60.0%; Pred. No. 6.3e+05;
Matches 27; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Oy 82 CCCCAGGCTGTGAGTTGCTCGCGCGCCCGCCGCGATGCGCATG 126
||||| ||| || || || || || || || || || || || || || ||
Db 50 CCCCAGGCTCCAGCTTGTGCGCNCNCNNNNNNCGCTCTCCCTG 6

RESULT 9
AZ993993
LOCUS         AZ993993 46 bp DNA linear GSS 27-APR-2001
DEFINITION   2M0279E13P Mouse 10kb plasmid DuCC2M library MUS musculus genomic
            clone DuCC2M0279E13 P, DNA sequence.
ACCESSION   AZ993993
VERSION     AZ993993.1  GI:13865220
KEYWORDS    GSS.
SOURCE      house mouse.

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/issue_type="moderately-differentiated adenocarcinoma"  
/tab_host="DH10B"  
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Salt;  
Site_2: NCI; Cloned unidirectionally. Primer: Oligo dr.  
Average insert size 1.7 kb. Life Technologies catalog #: 11531-019"
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ORIGIN				

Query Match 1.1%; Score 20; DB 9; Length 40;  
Best Local Similarity 72.2%; Pred. No. 1e+06;  
Matches 26; Conservative 0; Mismatches 10; Indels

QY 232 GGTGGTGGGGCAATGACCTGGAGAGGCCCCC 267  
||||| | | ||||| | |||||  
Db 39 GGTGGTGGTGTCTTTACCAACCTGGTGACCCCCC 4

Search completed: March 4, 2003, 00:50:32  
Job time : 2635 secs

GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 3, 2003, 22:39:05 : Search time 133 Seconds  
(without alignments)  
8182.066 Million cell updates/sec

Title: US-10-017-621-3

Perfect score: 1745  
Sequence: 1 tgggaagcagctaaaggatg.....gttcaactgccacttgctc 1745

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Capext 1.0

Searched: 460893 seqs, 311809382 residues

Total number of hits satisfying chosen parameters: 254638

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA.\*

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- 2: /cgn2\_6/ptodata/2/pubpna/PTCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/2/pubpna/PTCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	21.8	1.2	48	9 US-10-054-444-6	Sequence 6, Appl
2	21.6	31	10	US-09-801-274-752	Sequence 752, App
3	21.4	1.2	45	9 US-10-029-413A-25	Sequence 25, Appl
4	21	31	10	US-09-801-274-94	Sequence 94, Appl
5	20.4	1.2	48	9 US-09-943-722-47	Sequence 47, Appl
6	20	1.1	45	10 US-09-147-142-11	Sequence 11, Appl
7	20	1.1	45	10 US-09-147-142-12	Sequence 12, Appl
8	19.8	1.1	40	10 US-09-263-959-758	Sequence 758, App
9	19.6	1.1	42	10 US-09-790-417-235	Sequence 235, App
10	19.4	1.1	45	12 US-10-073-256-27	Sequence 27, Appl
11	19.4	1.1	45	12 US-10-073-256-35	Sequence 35, Appl
12	19.2	1.1	31	10 US-09-801-274-517	Sequence 517, App
13	19.2	1.1	46	10 US-09-263-959-121	Sequence 121, App
14	19	1.1	43	9 US-09-376-940-23	Sequence 23, Appl
15	19	1.1	45	10 US-09-818-066-32	Sequence 32, Appl
16	19	1.1	47	9 US-10-118-231-9	Sequence 9, Appl
17	18.8	1.1	48	9 US-09-840-277-104	Sequence 104, App
18	18.8	1.1	48	9 US-09-840-277-105	Sequence 105, App
19	18.8	1.1	48	10 US-09-753-436-67	Sequence 67, Appl

Sequence 107, App  
Sequence 15295, A  
Sequence 3433, Ap  
Sequence 5256, Ap  
Sequence 18, Appl  
Sequence 31, Appl  
Sequence 31, Appl  
Sequence 9, Appl  
Sequence 233, App  
Sequence 4, Appl  
Sequence 8, Appl  
Sequence 10, Appl  
Sequence 14, Appl  
Sequence 16, Appl  
Sequence 3236, Ap  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 25, Appl  
Sequence 24, Appl  
Sequence 25, Appl  
Sequence 33, Appl  
Sequence 34, Appl  
Sequence 3267, Ap  
Sequence 3311, Ap  
Sequence 3491, Ap

9 US-09-840-277-107  
25 10 US-09-866-108-15295  
22 18.6 1.1 48 9 US-09-864-785-3433  
23 18.4 1.1 41 9 US-09-938-842A-5256  
24 18.4 1.1 48 10 US-09-761-534A-18  
25 18.2 1.0 36 9 US-10-219-248-31  
26 18.2 1.0 36 9 US-10-219-247-31  
27 18.2 1.0 36 10 US-09-853-723-31  
28 18.2 1.0 50 9 US-09-943-722-9  
29 18 1.0 42 10 US-09-790-417-233  
30 18 1.0 43 12 US-10-043-142-4  
31 18 1.0 46 9 US-10-026-914-8  
32 18 1.0 46 9 US-10-026-914-10  
33 18 1.0 46 9 US-10-026-914-16  
34 18 1.0 46 9 US-09-864-785-3226  
35 18 1.0 48 9 US-10-051-989-2  
36 17.8 1.0 35 9 US-09-861-097-2  
37 17.8 1.0 42 10 US-09-865-807-25  
38 17.8 1.0 45 12 US-10-073-256-24  
39 17.8 1.0 45 12 US-10-073-256-25  
40 17.8 1.0 45 12 US-10-073-256-33  
41 17.8 1.0 45 12 US-10-073-256-34  
42 17.8 1.0 48 9 US-09-864-785-3267  
43 17.8 1.0 48 9 US-09-864-785-3311  
44 17.8 1.0 48 9 US-09-864-785-3491  
45 17.8 1.0 48 9 US-09-864-785-3491

## ALIGNMENTS

RESULT 1  
US-10-054-444-6  
; Sequence 6, Application US/10054444  
; Patent No. US20020164342A1  
; GENERAL INFORMATION:  
; APPLICANT: Guyre, Paul M.  
; APPLICANT: Goldstein, Joel  
; APPLICANT: Wu, Zining  
; APPLICANT: Sun, Wanwen  
; TITLE OF INVENTION: Recombinant Cat Allergen, Fel d1, Expressed In  
; TITLE OF INVENTION: Baculovirus for Diagnosis and Treatment of Cat Allergy  
; FILE REFERENCE: DC-0118  
; CURRENT APPLICATION NUMBER: US/10/054,444  
; PRIOR FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/410,963  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-10-05  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 48  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-054-444-6

Query Match 1.2% Score 21.8; DB 9;  
Best Local Similarity 70.7%; Pred. No. 9.5e+03;  
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 962 AGAAGTGCTACACCGACCTCAAGCCCGACAGACCTCTC 1002  
DB 2 AGAAGCTCTCCAGACCTCTCTCCACGAGACCTCTC 42

RESULT 2  
US-09-801-274-752  
; Sequence 752, Application US/09801274  
; Patent No. US2002032319A1  
; GENERAL INFORMATION:  
; APPLICANT: Cargill, Michele  
; APPLICANT: Ireland, James S.

RESULT 4  
US-09-801-274-94  
Sequence 94, Application US/09801274  
Patent No. US20020323194  
GENERAL INFORMATION:  
APPLICANT: Cargill, Michele  
APPLICANT: Ireland, James S.  
APPLICANT: Lander, Eric S.  
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS  
FILE REFERENCE: 2825.2009-001  
CURRENT APPLICATION NUMBER: US/09/801.274  
CURRENT FILING DATE: 2001-03-07  
PRIOR APPLICATION NUMBER: US 60/187.510  
PRIOR FILING DATE: 2000-03-07

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: PRIOR APPLICATION NUMBER: US 60/206,129
: PRIOR FILING DATE: 2000-05-22
: NUMBER OF SEQ ID NOS: 1802
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 94
: LENGTH: 31
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-801-774-94

Query Match          1.2k: Score 21: DB 10: Length 31:
Best Local Similarity 77.4k: Pred. No. 1.3e+04:
Matches 24: Conservative 1: Mismatches 6: Indels

QY 577 GTCAGCCTATCTGAGATTGCTTTGGGAAC 607
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DB 1 GCCTCCCTGTCAGACMTTGGCTTTGGGAAC 31

RESULT 5
US-09-943-722-47
: Sequence 47, Application US/09943722
: Publication No. US20020192660A1
: GENERAL INFORMATION:
: APPLICANT:
: APPLICANT:
: APPLICANT:
: TITLE OF INVENTION: METHOD OF ELIMINATING
: TITLE OF INVENTION: INHIBITORY/INSTABILITY REGIONS OF mRNA
: NUMBER OF SEQUENCES: 130
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORGAN & FINNEGAN
: STREET: 345 PARK AVENUE
: CITY: NEW YORK
: STATE: NEW YORK
: COUNTRY: USA
: ZIP: 10154
: COMPUTER READABLE FORM:
: MEDIUM TYPE: FLOPPY DISK
: COMPUTER: IBM PC COMPATIBLE
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WORDPERFECT 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/943,722
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/850,049
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/050,478
: FILING DATE: 26-OCT-1994
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/02908
: FILING DATE: 29-MAR-1993
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/856,747
: FILING DATE: 27-MAR-1992
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: MORRI, MARY J.
: REGISTRATION NUMBER: 34,398
: REFERENCE/DOCKET NUMBER: 2026-4006US1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212)758-4800
: TELEFAX: (212)751-6849
: INFORMATION FOR SEQ ID NO: 47:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 48 BASE PAIRS
: TYPE: NUCLEIC ACID
: STRANDEDNESS: SINGLE

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TOPOLOGY: LINEAR  
US-09-943-722-47

Query Match 1.18; Score 20.4; DB 9; Length 48;  
Best Local Similarity 71.18; Pred. No. 2.3e+04;  
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 325 GAGATTGTCACGAGGACTTGAAGATGGGTCTGATGG 362  
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Db 7 GAGACGGTGGCCGGAAGTTGAAGCCGGGATGATGG 44

RESULT 6

US-09-147-142-11  
Sequence 11 Application US/09147142  
Patent No. US20020018749A1  
GENERAL INFORMATION:  
APPLICANT: HUDSON, Peter John  
APPLICANT: KORTT, Alex Andrew  
APPLICANT: IRVING, Robert Alexander  
APPLICANT: ATWELL, John Leslie  
TITLE OF INVENTION: HIGH AVIDITY POLYVALENT AND POLYSPECIFIC REAGENTS  
FILE REFERENCE: 016786/0212  
CURRENT APPLICATION NUMBER: US/09/147,142  
CURRENT FILING DATE: 1999-03-05  
EARLIER APPLICATION NUMBER: PCT/AU98/00212  
EARLIER FILING DATE: 1998-03-26  
EARLIER APPLICATION NUMBER: AU PO 5917  
EARLIER FILING DATE: 1997-03-27  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 11  
LENGTH: 45  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
OTHER INFORMATION: oligonucleotide used to insert codon between VH  
OTHER INFORMATION: and VL domains of NC10 scfv-0  
US-09-147-142-11

Query Match 1.18; Score 20; DB 10; Length 45;  
Best Local Similarity 65.98; Pred. No. 2.8e+04;  
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 643 GGTACCTATCCACCGCTACAAAGGCAAGCAAGCTCACAGA 686  
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Db 1 GGGACACCGTCACCGCTCCGGTGGTATCGAGCTCACACA 44

RESULT 7

US-09-147-142-12/c  
Sequence 12 Application US/09147142  
Patent No. US20020018749A1  
GENERAL INFORMATION:  
APPLICANT: HUDSON, Peter John  
APPLICANT: KORTT, Alex Andrew  
APPLICANT: IRVING, Robert Alexander  
APPLICANT: ATWELL, John Leslie  
TITLE OF INVENTION: HIGH AVIDITY POLYVALENT AND POLYSPECIFIC REAGENTS  
FILE REFERENCE: 016786/0212  
CURRENT APPLICATION NUMBER: US/09/147,142  
CURRENT FILING DATE: 1999-03-05  
EARLIER APPLICATION NUMBER: PCT/AU98/00212  
EARLIER FILING DATE: 1998-03-26  
EARLIER APPLICATION NUMBER: AU PO 5917  
EARLIER FILING DATE: 1997-03-27  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 12  
LENGTH: 45  
TYPE: DNA  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
OTHER INFORMATION: oligonucleotide used to insert codon between VH  
OTHER INFORMATION: and VL domains of NC10 scfv-0  
US-09-147-142-12

Query Match 1.18; Score 20; DB 10; Length 45;  
Best Local Similarity 65.98; Pred. No. 2.8e+04;  
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 643 GGTACCTATCCACCGCTACAAAGGCAAGCAAGCTCACAGA 686  
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Db 45 GGGACACCGTCACCGCTCCGGTGGTATCGAGCTCACACA 2

RESULT 8

US-09-263-959-758  
Sequence 758 Application US/09163959  
Patent No. US20020150891A1  
GENERAL INFORMATION:  
APPLICANT: Hood, Leroy E.  
APPLICANT: ROVEN, Lee  
APPLICANT: KOOP, Ben F.  
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH U  
NUMBER OF SEQUENCES: 1279  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/09/263,959  
FILING DATE: 05-MAR-1999  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: McMaisters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 920010.426C2  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-8031  
INFORMATION FOR SEQ ID NO: 758:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-263-959-758

Query Match 1.18; Score 19.8; DB 10; Length 40;  
Best Local Similarity 77.48; Pred. No. 3e+04;  
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1689 CTTCCTCTGCTTACTCTCTGCTACCTGCTGCTG 1719  
||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 3 CTTCCTCTCTCTCTCTCTCTCTCTCTCTCTGCTGCTG 33

RESULT 9

US-09-790-417-235/c  
Sequence 235 Application US/09790417  
Patent No. US20010031470A1  
GENERAL INFORMATION:  
APPLICANT: Shultz, John W  
APPLICANT: Lewis, Martin K.  
APPLICANT: Lieppe, Donna



```
; APPLICANT: Mandrekar, Michelle
; APPLICANT: Kephart, Daniel
; APPLICANT: Rhodes, Richard B.
; APPLICANT: Andrews, Christine A.
; APPLICANT: Hartnett, James R.
; APPLICANT: Gu, Trent
; APPLICANT: Olson, Ryan J.
; APPLICANT: Wood, Keith W.
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: Nucleic Acid Detection
; FILE REFERENCE: Pro-103 6868/75528
; CURRENT APPLICATION NUMBER: US/09/790,417
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 05/358,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 05/042,287
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 235
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:probe for oligo
; OTHER INFORMATION: 54
US-09-790-417-235

Query Match 1.1%; Score 19.6; DB 10; Length 42;
Best Local Similarity 66.7%; Pred. No. 3.5e+04;
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 759 GTCCCTGCTCAAGGACCTCAACACGCGCCAACTCGTTACGCT 800
DB 42 CTACCTGCTAAATGAAGTCAACCCACGATATCATCAAGCT 1

RESULT 10
US-10-073-256-27/c
; Sequence 27, Application US/10073256
; Patent No. US20020120408A1
; GENERAL INFORMATION:
; APPLICANT: Kreiswirth, Barry M
; APPLICANT: Nadlich, Steven M
; TITLE OF INVENTION: System and Method for Tracking and Controlling Infections
; FILE REFERENCE: 19124.0002
; CURRENT APPLICATION NUMBER: US/10/073,256
; CURRENT FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-10-073-256-27

Query Match 1.1%; Score 19.4; DB 10; Length 45;
Best Local Similarity 64.4%; Pred. No. 4.1e+04;
Matches 29; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1288 ATCTGTCCACGAGGAGTTCAAGACATACAACTACCCCAAGTAC 1332
DB 45 AACCGAGGAACCACTAGTACCCAGGAGGAGGAGTACCTCAAGTAC 1

RESULT 11
US-10-073-256-35/c
; Sequence 35, Application US/10073256
; Patent No. US20020120408A1
; GENERAL INFORMATION:
; APPLICANT: Kreiswirth, Barry M
; APPLICANT: Nadlich, Steven M
; TITLE OF INVENTION: System and Method for Tracking and Controlling Infections
```

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; FILE REFERENCE: 19124.0002
; CURRENT APPLICATION NUMBER: US/10/073,256
; CURRENT FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-10-073-256-35

Query Match 1.1%; Score 19.4; DB 12; Length 45;
Best Local Similarity 64.4%; Pred. No. 4.1e+04;
Matches 29; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1288 ATCTGTCCACGAGGAGTTCAAGACATACAACTACCCCAAGTAC 1332
DB 45 AACCGAGGAACCACTAGTACCCAGGAGGAGGAGTACCTCAAGTAC 1

RESULT 12
US-09-801-274-517
; Sequence 517, Application US/09801274
; Patent No. US20020032319A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.2009-001
; CURRENT APPLICATION NUMBER: US/09/801,274
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 1802
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 517
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-274-517

Query Match 1.1%; Score 19.2; DB 10; Length 31;
Best Local Similarity 80.8%; Pred. No. 3.9e+04;
Matches 21; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1190 CCACAGGCGGTCCCTCTTTCCGGGC 1215
DB 5 CCACAGGCGTTCCCTCTTCGTGGGC 30

RESULT 13
US-09-263-959-121/c
; Sequence 121, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH U
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```









```

: APPLICANT: Cantor, Charles R.
: APPLICANT: Andrews, Beth M.
: APPLICANT: Turin, Lisa M.
: APPLICANT: Fry, Kirk E.
: TITLE OF INVENTION: Sequence-Directed DNA Binding
: TITLE OF INVENTION: Molecules, Compositions and Methods
: NUMBER OF SEQUENCES: 664
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genelabs Technologies, Inc.
: STREET: 505 Penobscot Drive
: CITY: Redwood City
: STATE: CA
: COUNTRY: USA
: ZIP: 94063
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/482,080A
: FILING DATE: 07-JUN-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/171,389
: FILING DATE: 20-DEC-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/123,936
: FILING DATE: 17-SEP-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/996,783
: FILING DATE: 23-DEC-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/723,618
: FILING DATE: 27-JUN-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/081,070
: FILING DATE: 22-JUN-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Brady, John F.
: REGISTRATION NUMBER: 39,118
: REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (650) 324-0880
: TELEFAX: (650) 324-0960
: INFORMATION FOR SEQ ID NO: 156:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 46 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ORIGINAL SOURCE:
: INDIVIDUAL ISOLATE: Human H1 histone gene PNC16
: US-08-482-080A-156

Query Match 1.28; Score 21.4; DB 3; Length 46;
Best Local Similarity 71.84; Pred. No. 9.3e+03;
Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1641 GCGGCTGGAGGATGCCACACCCCTCACAGGCGAGCC 1679
      ||||| ||||| ||||| ||||| ||||| ||||| ||
DB 2 GCGGTGGATTGGACGCTCCACCAATCACAGGCGAGCC 40

RESULT 8
US-09-354-947-156
: Sequence 156, Application US/09354947
: Patent No. 6384208
: GENERAL INFORMATION:
: APPLICANT: Edwards, Cynthia A.
: APPLICANT: Cantor, Charles R.
: APPLICANT: Andrews, Beth M.
: TITLE OF INVENTION: Sequence-Directed DNA Binding
: TITLE OF INVENTION: Molecules, Compositions and Methods
: NUMBER OF SEQUENCES: 641
```

```

: APPLICANT: Turin, Lisa M.
: APPLICANT: Fry, Kirk E.
: TITLE OF INVENTION: Sequence-Directed DNA Binding
: TITLE OF INVENTION: Molecules, Compositions and Methods
: NUMBER OF SEQUENCES: 664
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genelabs Technologies, Inc.
: STREET: 505 Penobscot Drive
: CITY: Redwood City
: STATE: CA
: COUNTRY: USA
: ZIP: 94063
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/354,947
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/482,080
: FILING DATE: 07-JUN-1995
: APPLICATION NUMBER: US 08/171,389
: FILING DATE: 20-DEC-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/123,936
: FILING DATE: 17-SEP-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/996,783
: FILING DATE: 23-DEC-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/723,618
: FILING DATE: 27-JUN-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/081,070
: FILING DATE: 22-JUN-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Brady, John F.
: REGISTRATION NUMBER: 39,118
: REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (650) 324-0880
: TELEFAX: (650) 324-0960
: INFORMATION FOR SEQ ID NO: 156:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 46 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ORIGINAL SOURCE:
: INDIVIDUAL ISOLATE: Human H1 histone gene PNC16
: US-09-354-947-156

Query Match 1.28; Score 21.4; DB 4; Length 46;
Best Local Similarity 71.84; Pred. No. 9.3e+03;
Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1641 GCGGCTGGAGGATGCCACACCCCTCACAGGCGAGCC 1679
      ||||| ||||| ||||| ||||| ||||| ||||| ||
DB 2 GCGGTGGATTGGACGCTCCACCAATCACAGGCGAGCC 40

RESULT 9
PCT-US93-12388-156
: Sequence 156, Application PC/TUS9312388
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: Sequence-Directed DNA Binding
: TITLE OF INVENTION: Molecules, Compositions and Methods
: NUMBER OF SEQUENCES: 641
```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12388
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175.41/G19PCT2
TELEPHONE: (415) 324-0860
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 156:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human H1 histone gene FNC16
PCT-US93-12388-156

```

```

Query Match 1.2% Score 21.4; DB 5; Length 46;
Best Local Similarity 71.8%; Pred. No. 9.3e+03;
Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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```

Oy 1641 GCGGTGGAGGATCCACACCTCCACAGGCGGCC 1679
      |||| | ||| || |||| ||||| ||||| |||
Db 2 GCGGTGATTGACCTCCACCAATCACAGGCGGCC 40

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RESULT 10
US-08-233-009-33
Sequence 33, Application US/08233009
Patent No. 5646156
GENERAL INFORMATION:
APPLICANT: Jacobson, Marlene A
APPLICANT: Johnson, Robert G
APPLICANT: Salvatore, Christopher A
TITLE OF INVENTION: INHIBITION OF EOSINOPHIL
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: United States
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

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```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,009
FILING DATE: 25-APR-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H.
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: 19219
TELEPHONE: (908) 594-3901
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-233-009-33

```

```

Query Match 1.2% Score 20.6; DB 1; Length 45;
Best Local Similarity 67.4%; Pred. No. 1.5e+04;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

```

```

Oy 737 CTTGCACCCCATCCGGAGCTGCTCCTGCTCAGGACCTCAA 779
      ||||| |||| | || |||| ||||| |||||
Db 2 CTTGCACCCCATCTTAGCCCCCTGCCNAGGTATCCA 44

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```

RESULT 11
US-08-285-936-38/c
Sequence 38, Application US/08285936
Patent No. 5728821
GENERAL INFORMATION:
APPLICANT: Yelton, Dale
APPLICANT: Glaser, Scott
APPLICANT: Huse, William
APPLICANT: Rosok, Mae J.
TITLE OF INVENTION: No. 5728821el Mutant BR96 Antibodies and
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90025-3395
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/285,936
FILING DATE: 04-AUG-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436.16US01
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

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;; MEDIUM TYPE: FLOPPY DISK  
;; COMPUTER: IBM PC COMPATIBLE  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: WORDPERFECT 5.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/050,478  
;; FILING DATE: 26-OCT-1994  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US93/07908  
;; FILING DATE: 29-MAR-1993  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/858,747  
;; FILING DATE: 27-MAR-1992  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: MORRY, MARY J.  
;; REGISTRATION NUMBER: 34,398  
;; REFERENCE/DOCKET NUMBER: 2026-40060S1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212)751-6849  
;; TELEFAX: (212)751-6849  
;; INFORMATION FOR SEQ ID NO: 47:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 48 BASE PAIRS  
;; TYPE: NUCLEIC ACID  
;; STRANDEDNESS: SINGLE  
;; TOPOLOGY: LINEAR  
US-08-050-478-47

Query Match 1.2% Score 20.4; DB 2; Length 48;  
Best Local Similarity 71.1%; Pred. No. 1.7e+04;  
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Oy 325 GAGATTGTGCACGAGGACTTGAAGATGGGGTCTGATCG 362  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 7 GACACGGTCCCGCTGAAGTTGAAGCCGGGGATGATCG 44

## RESULT 15

US-09-414-117-47  
;; Sequence 47, Application US/09414117  
;; Patent No. 6291664  
;; GENERAL INFORMATION:  
;; APPLICANT:  
;; APPLICANT:  
;; TITLE OF INVENTION: METHOD OF ELIMINATING  
;; TITLE OF INVENTION: INHIBITORY/INSTABILITY REGIONS OF mRNA  
;; NUMBER OF SEQUENCES: 130  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: MORGAN & FINNEGAN  
;; STREET: 345 PARK AVENUE  
;; CITY: NEW YORK  
;; STATE: NEW YORK  
;; COUNTRY: USA  
;; ZIP: 10154  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: FLOPPY DISK  
;; COMPUTER: IBM PC COMPATIBLE  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: WORDPERFECT 5.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/414,117  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/850,049  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US93/02908

;; FILING DATE: 29-MAR-1993  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/858,747  
;; FILING DATE: 27-MAR-1992  
;; CLASSIFICATION:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: MORRY, MARY J.  
;; REGISTRATION NUMBER: 34,398  
;; REFERENCE/DOCKET NUMBER: 2026-40060S1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212)751-6849  
;; TELEFAX: (212)751-6849  
;; INFORMATION FOR SEQ ID NO: 47:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 48 BASE PAIRS  
;; TYPE: NUCLEIC ACID  
;; STRANDEDNESS: SINGLE  
;; TOPOLOGY: LINEAR  
US-09-414-117-47

Query Match 1.2% Score 20.4; DB 4; Length 48;  
Best Local Similarity 71.1%; Pred. No. 1.7e+04;  
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Oy 325 GAGATTGTGCACGAGGACTTGAAGATGGGGTCTGATCG 362  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 7 GACACGGTCCCGCTGAAGTTGAAGCCGGGGATGATCG 44

Search completed: March 4, 2003, 00:52:00  
Job time : 80 secs

GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run On: March 3, 2003, 19:29:35 ; Search time 427 Seconds  
(without alignments)  
9203.131 Million cell updates/sec

Title: US-10-017-621-3  
Perfect score: 1745  
Sequence: 1 tggagacagcgttaagatg.....gtccacccctccactgtcc 1745

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues  
Total number of hits satisfying chosen parameters: 2156140

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :	N_Geneseq_101002:*
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3:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:*
4:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:*
5:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:*
6:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:*
7:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1986.DAT:*
8:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1987.DAT:*
9:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:*
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11:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1990.DAT:*
12:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1991.DAT:*
13:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1992.DAT:*
14:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:*
15:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1994.DAT:*
16:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1995.DAT:*
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18:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:*
19:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:*
20:	/SID52/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:*
21:	/SID52/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:*
22:	/SID52/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:*
23:	/SID52/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*
24:	/SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	24.8	1.4	50	22	Human SNP oligonuc
C 2	22.4	1.3	33	24	Human Cdk5 related
C 3	22.4	1.3	33	24	Human Cdk5 related
C 4	22	1.3	31	22	Human single nucle
C 5	22	1.3	31	22	Human single nucle
C 6	21.4	1.2	31	22	Human single nucle
C 7	21.4	1.2	42	22	PCR primer SR53 fo
C 8	21.4	1.2	42	24	ifnG coding region
C 9	21.4	1.2	46	15	Human H1 histone g

10	21.4	1.2	46	18	AAT63868	Human H1 histone g
11	21.4	1.2	46	20	AA17156	Test sequence from
12	21.4	1.2	46	24	ABK82647	DNA binding molecu
13	21	1.2	21	22	AAH62195	CTA18G-1 polymorp
C 14	21	1.2	46	22	AAH70659	Human cervical can
C 15	21	1.2	50	22	AA134286	Human SNP oligonuc
C 16	20.8	1.2	46	20	AA123932	DE19736331 primer
C 17	20.6	1.2	45	16	AA107598	RT-PCR primer/prob
C 18	20.6	1.2	45	16	AA107598	Primer 143 for hum
C 19	20.6	1.2	50	22	AA127875	Human SNP oligonuc
C 20	20.4	1.2	32	24	AA172077	Human SNP oligonuc
C 21	20.4	1.2	48	14	AAQ50230	Xcds1 degenerate p
C 22	20.2	1.2	36	19	AAV46356	HIV pol INS mutag
C 23	20.2	1.2	40	16	AAQ76190	PCR primer for ser
C 24	20.2	1.2	40	18	AA191033	Primer for amplif
C 25	20.2	1.2	40	24	ABL54053	Human 4-1BB 3' PCR
C 26	20.2	1.2	40	24	ABK48669	Human cytokine rec
C 27	20.2	1.2	41	24	ABK48669	Human proton-aden
C 28	20.2	1.2	45	22	AA172870	Human proton-aden
C 29	20.2	1.2	49	20	AA131379	MUSIGHAEI Mouse Ig
C 30	20.2	1.2	50	19	AAV59127	Reverse PCR primer
C 31	20.2	1.2	50	22	AA135338	Reverse PCR primer
C 32	20	1.1	41	19	AAV37843	CD4+ human T-lymph
C 33	20	1.1	41	24	AA134819	Human large protei
C 34	20	1.1	46	21	AA291309	IL-6R and IL-6 fus
C 35	20	1.1	47	21	AA267885	Human map-related
C 36	20	1.1	50	22	AA129783	Human SNP oligonuc
C 37	20	1.1	50	22	AA134645	Human SNP oligonuc
C 38	19.8	1.1	46	21	AA102589	Hammerhead ribozym
C 39	19.8	1.1	48	18	AA176036	Human A2B adenosin
C 40	19.8	1.1	48	20	AA135859	Human adenosine A2
C 41	19.8	1.1	48	21	AA19424	Human adenosine A2
C 42	19.8	1.1	48	21	AA133302	Low adenosine anti
C 43	19.8	1.1	48	21	AA133302	Low adenosine anti
C 44	19.8	1.1	48	21	AA133302	Low adenosine anti
C 45	19.6	1.1	31	22	AA130029	Nucleotide sequenc

## ALIGNMENTS

RESULT 1	
AA134335/c	
ID	AA134335 standard; DNA; 50 BP.
XX	AA134335;
XX	AA134335;
XX	24-JAN-2002 (first entry)
XX	Human SNP oligonucleotide #7543.
XX	Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX	neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
XX	anyoid protein; angiopoietin; apoptosis related protein; cadherin;
XX	cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
XX	complement related protein; cytochrome; kinesin; cytokine; interferon;
XX	interleukin; G-protein coupled receptor; thioesterase; inflammation;
XX	multifactorial disease; autoimmune disease; infection;
XX	nervous system disease; ss.
OS	Homo sapiens.
XX	WO200147944-A2.
XX	05-JUL-2001.
XX	28-DEC-2000; 2000WO-US35498.
XX	28-DEC-1999; 99US-0173419.
XX	27-DEC-2000; 2000US-0173419.
XX	(CURA-) CURAGEN CORP.



```

Query Match      1.3%; Score 22.4; DB 24; Length 33;
Best Local Similarity 81.2%; Pred. No. 2.8e+04;
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1018 GAGCTCAAGCTGCGTCTTGGCGTGGCCG 1049
      IIII I IIII I IIII IIII I I
Db 32 GAGCTGAATGCTCAATTTGGCGTGGCTCG 1

RESULT 4
AAI30264
ID AAI30264 standard; DNA: 31 BP.
XX
AC AAI30264;
XX
DT 18-OCT-2001 (first entry)
XX
DE Human single nucleotide polymorphism (SNP) 97.
XX
KW Human; resequencing; genotype; disease; forensic; paternity testing;
KW single nucleotide polymorphism; SNP; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Variation replace(16,T)
FT FT /tag= a
FT FT /standard_name= "single nucleotide polymorphism"
XX
PN WO200166800-A2.
XX
PD 13-SEP-2001.
XX
PF 07-MAR-2001; 2001WO-US07268.
XX
PR 07-MAR-2000; 2000US-0187510.
XX
PR 22-MAY-2000; 2000US-0206129.
XX
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI Cargill M, Ireland JS, Lander ES;
XX
PFI 2001-522952/57.
XX
DR Nucleic acid molecules from the human genome which include polymorphic
PT sites, useful in methods for predicting the presence, absence or
PT severity of a particular phenotype or disorder (e.g. diabetes)
PT associated with a particular genotype -
XX
PS Claim 1; Page 75; 145pp; English.
XX
CC The invention relates to the identification of nucleic acid molecules
CC (AAI29513-AAI3114) from the human genome which include polymorphic sites
CC which can predispose individuals to disease. Various genes from a number
CC of individuals were resequenced and single nucleotide polymorphisms
CC (SNPs) in these genes discovered. The method is useful for predicting the
CC presence, absence or severity of a particular phenotype or disorder (e.g.
CC diabetes) associated with a particular genotype. The nucleic acids
CC containing the polymorphic sites may be useful in forensics and paternity
CC testing.
XX
SQ Sequence 31 BP; 8 A; 11 C; 8 G; 4 T; 0 other;

Query Match      1.3%; Score 22; DB 22; Length 31;
Best Local Similarity 83.3%; Pred. No. 3.4e-04;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 979 GACCTCAAGCCCGCAGACCTGCTCATCAAC 1008
      III IIIII IIIII IIIII I I I
Db 2 GACATCAAGCCCGCAGACCTGCTGTGGAC 31

```

```

RESULT 5
AAI75839
ID AAI75839 standard; DNA: 50 BP.
XX
AC AAI75839;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:2780.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
OS Homo sapiens.
XX
PN WO200140521-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WO-US32758.
XX
PR 30-NOV-1999; 99US-0168138.
PR 29-NOV-2000; 2000US-0726173.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shinkets RA, Leach M;
XX
PFI 2001-356160/37.
XX
DR Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy -
XX
PS Claim 1; Page 901; 2653pp; English.
XX
CC AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AAI53114 to AAI53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides.
CC For example, (I) may be used to treat disorders by rectifying mutations
CC or deletions in a patient's genome that affect the activity of
CC polypeptides by expressing inactive proteins or to supplement the
CC patients own production of polypeptide. Additionally, (I) and its
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acids
CC in samples, and therefore which patients may be in need of restorative
CC therapy. The polypeptides encoded by (I) may be used as antigens in the
CC production of antibodies specific for polymorphic polypeptides. The
CC antibodies may also be used to down regulate expression and activity.
CC The antibodies may also be used as diagnostic agents for detecting the
CC presence of polymorphic polypeptides in samples.
XX
SQ Sequence 50 BP; 7 A; 22 C; 13 G; 8 T; 0 other;

Query Match      1.3%; Score 22; DB 22; Length 50;
Best Local Similarity 73.7%; Pred. No. 4.2e+04;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 1642 CGCGTGGAGGATGCCACACCCCTCACAGGCGGCC 1679
      III III I IIIII IIIII I I I
Db 11 CTGCTTGAAGCGTGGCAGACCCCTCTCTGTGGGCCCCC 48

RESULT 6
AAI29606
ID AAI29606 standard; DNA: 31 BP.
XX
AC AAI29606;
XX

```



XX DR WPI; 2002-171810/22.

XX PS Producing a protein of interest, e.g., a pharmaceutically active

XX PT protein, comprises expressing a polynucleotide fusion construct in a

XX PT plasmid and producing a fusion protein comprising the protein of

XX PT interest.

XX PS Example 1; Page 90; 92pp; English.

XX CC The patent discloses a method of producing a protein of interest which

XX CC involves expressing a polynucleotide fusion construct in a plasmid to

XX CC produce a fusion protein comprising the protein of interest where the

XX CC construct comprises a polynucleotide coding sequence of the protein of

XX CC interest operably linked to a polynucleotide coding sequence of a fusion

XX CC protein partner. The methods of the invention are useful for producing a

XX CC protein of interest which comprises a human protein or its biologically

XX CC active variant or fragment, a pharmaceutically active protein, an IFN

XX CC (interferon), its biologically active variant or fragment, a human IFN-

XX CC gamma or its biologically active variant or fragment. They are useful

XX CC for the production of transgenic plants. Methods of the invention are

XX CC also useful for the generation of transplacental plant cells, plants

XX CC and seeds. The protein of interest obtained by the methods of the

XX CC invention is useful for the manufacture of a medicament for treating

XX CC a disease condition. The present DNA sequence is a PCR primer which

XX CC is used for amplifying ifnc coding region. This primer is used in

XX CC the exemplification of the invention to generate pcUSIFNG expression

XX CC vector for ifnc in chloroplasts.

XX SQ Sequence 42 BP; 15 A; 10 C; 11 G; 6 T; 0 other;

Query Match 1.24; Score 21.4; DB 24; Length 42;

Best Local Similarity 80.6%; Pred. No. 5.6e+04;

Matches 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 270 ACGTGTGCTCTCGGGCAACTGCTTCGCA 300

DB 35 ACGTAGGGTCTCGGCACCTTCGATCGCA 5

RESULT 9

AAQ69406

ID AAQ69406 standard; DNA: 46 BP.

XX AC AAQ69406;

XX DT 27-FEB-1995 (first entry)

XX DE Human H1 histone gene FNC16, target region.

XX KW DNA protein-binding assay; test sequence; screening sequence;

XX KW promoter; target; TATA box; Herpes Simplex Virus; HSV;

XX KW origin of replication; UL9; transcription factor; TFIIID; ds.

XX OS Synthetic.

XX PN MO9414980-A.

XX PD 07-JUL-1994.

XX PF 20-DEC-1993; 93MO-US12388.

XX PR 23-DEC-1993; 92US-0996783.

XX PR 17-SEP-1993; 93US-0123936.

XX PA (GENE-) GENELABS TECHNOLOGIES INC.

XX PI Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;

XX DR WPI; 1994-234711/28.

XX PT Sequence-directed DNA-binding molecules - useful in

XX PT pharmaceuticals and as molecular reagents

XX PS Claim 28; Page 290; 587pp; English.

XX CC A DNA protein-binding assay is provided, useful for screening

XX CC libraries of synthetic or biological cpds. for their ability

XX CC to bind DNA test sequences. The assay is versatile in that any

XX CC number of test sequences can be tested by placing the test sequence

XX CC adjacent to a defined protein-binding screening sequence. Binding

XX CC of mols. to these test sequences changes the binding characteristics

XX CC of the protein mol. to its cognate binding sequence. When such a mol.

XX CC binds the test sequence, the equilibrium of the DNA:protein complex

XX CC is disturbed, generating changes in the concentration of free DNA probe.

XX CC One application of this method is to eucaryotic general transcription

XX CC factors (e.g. TFIIID) where the target region is typically selected

XX CC from DNA sequences adjacent to the binding site for the eucaryotic

XX CC transcription factor. Numerous exemplary test sequences are given:

XX CC the sequences in AAQ69251-731 and AAQ69850 correspond to promoter

XX CC targets (typically, TATA box-contg. sites) for human genes and the

XX CC sequences in AAQ69732-849 correspond to promoter targets for viral

XX CC genes. The test sequences may also be randomly generated. DNA:protein

XX CC interaction may be used for screening purposes, e.g. the Herpes Simplex

XX CC Virus (HSV) origin of replication and UL9 (see AAQ69851-52, AAQ69865 and

XX CC AAQ69891).

XX SQ Sequence 46 BP; 9 A; 14 C; 16 G; 7 T; 0 other;

Query Match 1.24; Score 21.4; DB 15; Length 46;

Best Local Similarity 71.8%; Pred. No. 5.8e+04;

Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 1641 GCGGTGGAGGGATGCCACACCCCTCACAGGCGAGCC 1679

DB 2 GCGGTGGATGGACGCTCCACCAATCACAGGCGAGCC 40

RESULT 10

AAQ63868

ID AAQ63868 standard; DNA: 46 BP.

XX AC AAQ63868;

XX DT 14-MAR-1997 (first entry)

XX DE Human H1 histone gene FNC16 gene TFIIID binding site.

XX KW Duplex DNA; target region; binding characteristic; DNA binding protein;

XX KW TFIIID; transcription factor; binding site; inhibition; enhance;

XX KW cancer; inherited genetic disorder; alpha-D-galactosidase A; ds.

XX OS Homo sapiens.

XX PN US5578444-A.

XX PD 26-NOV-1996.

XX PF 27-JUN-1991; 91US-0723618.

XX PR 20-DEC-1993; 93US-0171389.

XX PR 27-JUN-1991; 91US-0723618.

XX PR 23-DEC-1992; 92US-0996783.

XX PR 17-SEP-1993; 93US-0123936.

XX PA (GENE-) GENELABS TECHNOLOGIES INC.

XX PI Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;

XX DR WPI; 1997-020402/02.

XX PT Altering binding characteristics of DNA binding proteins to duplex

XX PT DNA - by attaching specific small cpd. to target region close to the

XX PT protein's binding site, useful in treatment of viral disease, cancer

XX PT etc



XX Example 15; SEQ ID No 156; 98pp; English.

XX The invention relates to a method of decreasing transcriptional activity

CC in a duplex deoxyribonucleic acid (DNA) template (T1) comprising

CC contacting (T1) with a binding agent comprising at least one small duplex

CC DNA-binding molecule (T2) coupled to at least one other small duplex-

CC binding molecule that binds to a non-overlapping region of target

CC sequence (T3). The method is useful for inhibiting transcription of a

CC range of disease-related genes for treating infections (by viruses,

CC including human immunodeficiency virus, bacteria, fungi, protozoa

CC and parasites), cancer, cardiovascular, respiratory, gastrointestinal,

CC endocrine/metabolic, rheumatic/immunological, haematological,

CC neurologic, psychiatric, dermatological, ophthalmological,

CC musculo-skeletal, genetic or urogenital disorders. The method provides

CC sequence-specific inhibition of transcription of pathological genes

CC without affecting transcription of cellular genes regulated by the same

CC transcription factor, and can be applied to regulation of any gene.

CC A8K82492-A8K83155 represent DNA binding molecule test sequences used in

CC the method of the invention.

XX

XX Sequence 46 BP; 9 A; 14 C; 16 G; 7 T; 0 other;

XX

Query Match 1.2%; Score 21.4; DB 24; Length 46;

Best Local Similarity 71.8%; Pred. No. 5.8e+04;

Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1641 GCGGCTGAGGATGCCACACCCCTCACAGGCGAGCCCC 1679

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||

DB 2 GCGGTGATTGGACGCTCCCAATACACAGGCGAGCCCC 40

RESULT 13

AAH62195

ID AAH62195 standard; DNA: 21 BP.

AC AAH62195;

XX

DT 12-SEP-2001 (first entry)

XX

DE PCTAIRE-1 polymorphism containing DNA fragment #96.

XX

XX Single nucleotide polymorphism; SNP; human; cancer; inflammation;

KW heart disease; paternity testing; forensic science; ds.

XX

XX Homo sapiens.

XX

FT Key Location/Qualifiers

FT Variation replace(11,G)

FT /\*tag= a

FT /\*standard\_name= "single nucleotide polymorphism"

XX

PN WO200138576-A2.

XX

XX 31-MAY-2001.

XX

PF 17-NOV-2000; 2000WO-US31639.

XX

PR 24-NOV-1999; 99US-0167334.

XX

XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.

XX

PI Cargill M. Ireland JS, Lander ES;

XX

DR WPI: 2001-367705/38.

XX

XX New nucleic acid segments of the human genome, particularly from genes

PT including polymorphic sites, for phenotype correlation, forensics,

PT paternity testing, medicine and genetic analysis -

XX

XX Claim 1; Page 37; 80pp; English.

XX

XX DNA sequences AAH62100 - AAH62688 represent segments of human genes which

CC contain single nucleotide polymorphisms (SNPs). A method is included in

CC the invention for analysing a nucleic acid sample, which consists of

CC determining the base occupying any one of the polymorphic sites given in

CC the SNP containing sequences. The nucleotide sequences can be used in the

CC diagnosis or monitoring of diseases, such as cancer, inflammation, heart

CC diseases, diseases of the cardiovascular system, and infection by

CC microorganisms. The oligonucleotides are also useful in the manufacture

CC of a medicament for the treatment or prophylaxis of the diseases, and as

CC a pharmaceutical. SNP containing oligonucleotides are useful in

CC applications such as phenotype correlation, forensics, paternity testing,

CC medicine and genetic analysis.

XX

XX Sequence 21 BP; 9 A; 4 C; 6 G; 2 T; 0 other;

XX

Query Match 1.2%; Score 21; DB 22; Length 21;

Best Local Similarity 100.0%; Pred. No. 5.4e+04;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 702 CAAGGAGATCAGACTCGAACCA 722

||||| ||||| ||||| ||||| ||||| ||||| |||||

DB 1 CAAGGAGATCAGACTCGAACCA 21

RESULT 14

AAH70659/c

ID AAH70659 standard; cDNA: 46 BP.

AC AAH70659;

XX

DT 19-SEP-2001 (first entry)

XX

DE Human cervical cancer marker nucleic acid 1933.

XX

XX Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.

KW

XX Homo sapiens.

OS

PN WO200142467-A2.

XX

XX 14-JUN-2001.

XX

PF 08-DEC-2000; 2000WO-US33312.

XX

PR 08-DEC-1999; 99US-0169681.

XX

PR 21-DEC-1999; 99US-0171350.

XX

PR 14-MAR-2000; 2000US-0189315.

XX

PR 12-MAY-2000; 2000US-0203791.

XX

PR 09-JUN-2000; 2000US-0210600.

XX

XX 21-JUL-2000; 2000US-0220114.

XX

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX

PI Schlegel R, Deeds J, Berger A, Zhao X;

XX

DR WPI: 2001-375006/39.

XX

PT New isolated nucleic acid for diagnosing and treating cervical cancer

PT and for assessing and detecting compounds for treating the cancer -

XX

XX Claim 1; Page 415; 1051pp; English.

XX

XX The invention relates to novel genes (AAH68727-AAH73383) associated with

CC cervical cancer with cytostatic activity. The nucleic acids and encoded

CC polypeptides are useful: to assess if a patient is afflicted with

CC cervical cancer or has a pre-malignant condition; to monitor the

CC progression of cervical cancer or a premalignant condition in a patient;

CC and to select and/or assess the efficacy of a compound or therapy for

CC inhibiting cervical cancer in a patient. The nucleic acids may also be

CC useful for gene therapy.

XX

XX Sequence 46 BP; 7 A; 13 C; 18 G; 6 T; 2 other;

XX

XX Query Match 1.2%; Score 21; DB 22; Length 46;





GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sv model

Run on: March 3, 2003, 21:30:10 ; Search time 4788 Seconds  
(without alignments)  
10606.599 Million cell updates/sec

Title: US-10-017-621-3  
Perfect score: 1745  
Sequence: 1 tgaagcagcgtataagagatg.....gttcacactgcccactgtctc 1745

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb.ba.\*
- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pi.\*
- 9: gb.ro.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
- 16: em.fun.\*
- 17: em.hum.\*
- 18: em.in.\*
- 19: em.mu.\*
- 20: em.mu.\*
- 21: em.or.\*
- 22: em.ov.\*
- 23: em.pat.\*
- 24: em.ph.\*
- 25: em.pl.\*
- 26: em.ro.\*
- 27: em.sts.\*
- 28: em.un.\*
- 29: em.vi.\*
- 30: em.htg.hum.\*
- 31: em.htg.in.\*
- 32: em.htg.other.\*
- 33: em.htg.mus.\*
- 34: em.htg.pln.\*
- 35: em.htg.rod.\*
- 36: em.htg.mam.\*
- 37: em.htg.vrt.\*
- 38: em.sy.\*
- 39: em.htgo.hum.\*
- 40: em.htgo.mus.\*
- 41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
C	1	23.8	1.4	49	9	HSHCAK	X76171	H.sapiens m
	2	22.8	1.3	50	6	A93721	A93721	Sequence 8
	3	22.4	1.3	50	6	A93722	A93722	Sequence 9
	4	22.2	1.3	47	6	I84671	I84671	Sequence 5
	5	22	1.3	50	6	AX159452	AX159452	Sequence
	6	21.6	1.2	31	6	AX248673	AX248673	Sequence
C	7	21.4	1.2	42	6	AX182243	AX182243	Sequence
	8	21.4	1.2	42	6	AX382049	AX382049	Sequence
C	9	21.4	1.2	46	6	AR032544	AR032544	Sequence
	10	21.4	1.2	46	6	AR209208	AR209208	Sequence
	11	21.4	1.2	46	6	I29284	I29284	Sequence 15
	12	21.4	1.2	46	6	I30958	I30958	Sequence 15
	13	21	1.2	31	6	AX248015	AX248015	Sequence
C	14	21	1.2	46	6	AX186238	AX186238	Sequence
C	15	20.8	1.2	46	6	A96791	A96791	Sequence 24
	16	20.6	1.2	21	6	AX153998	AX153998	Sequence
C	17	20.6	1.2	45	6	AR022074	AR022074	Sequence
	18	20.6	1.2	45	6	I55009	I55009	Sequence 13
C	19	20.6	1.2	45	6	I32864	I32864	Sequence 18
	20	20.4	1.2	48	6	AR079723	AR079723	Sequence
	21	20.4	1.2	48	6	AR081253	AR081253	Sequence
	22	20.4	1.2	48	6	AR170613	AR170613	Sequence
	23	20.2	1.2	40	6	AR200128	AR200128	Sequence
	24	20.2	1.2	40	6	I88030	I88030	Sequence 13
C	25	20.2	1.2	43	6	AX225269	AX225269	Sequence
	26	20.2	1.2	49	6	AR083818	AR083818	Sequence
	27	20.2	1.2	49	9	S82032	S82032	Wtl-Wilms'
C	28	20.2	1.2	50	6	AX233404	AX233404	Sequence
	29	20	1.1	36	6	A07324	A07324	Synthetic D
	30	20	1.1	36	6	I12501	I12501	Sequence 18
	31	20	1.1	41	6	BD007098	BD007098	Targeted
C	32	20	1.1	44	6	A07325	A07325	Synthetic D
	33	20	1.1	44	6	I12502	I12502	Sequence 19
	34	20	1.1	46	6	E52011	E52011	IL-6 recept
	35	19.8	1.1	46	6	AX036348	AX036348	Sequence
	36	19.8	1.1	46	6	AX036350	AX036350	Sequence
C	37	19.8	1.1	48	6	BD012118	BD012118	Vitamin D
C	38	19.8	1.1	48	23	BD004595	BD004595	Sequence
	39	19.6	1.1	39	6	AX452342	AX452342	Sequence
C	40	19.6	1.1	42	6	AR153233	AR153233	Sequence
	41	19.6	1.1	45	6	I17261	I17261	Sequence 27
C	42	19.6	1.1	45	6	AR032970	AR032970	Sequence 19
	43	19.6	1.1	50	6	AR209634	AR209634	Sequence
	44	19.6	1.1	50	6	AX199648	AX199648	Sequence
	45	19.6	1.1	50	6	AX199648	AX199648	Sequence

ALIGNMENTS

RESULT 1  
HSHCAK HSHCAK 49 bp mRNA linear PRI 08-AUG-1995  
LOCUS H.sapiens mRNA for Cdk activating kinase.  
DEFINITION H.sapiens mRNA for Cdk activating kinase.  
ACCESSION X76171  
VERSION X76171.1 GI:429096  
KEYWORDS activating kinase; protein kinase.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 49)  
AUTHORS Hall F.L.  
TITLE Direct Submission  
JOURNAL Submitted (08-NOV-1993) F.L. Hall, Childrens Hospital Los Angeles,



REFERENCE 1 (bases 1 to 50)  
 AUTHORS Shimketa, R.A. and Leach, M.  
 TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof  
 JOURNAL Patent: WO 0140521-A 2780 07-JUN-2001.  
 FEATURES  
 source Location/Qualifiers  
 misc\_feature 1..50  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 25..26  
 /note="Nucleotide deleted between bases 25 and 26"  
 misc\_feature 26  
 Accession number CG42460243  
 BASE COUNT 7 a 22 c 13 g 8 t  
 ORIGIN  
 Query Match 1..38 Score 22; DB 6; Length 50;  
 Best Local Similarity 73.7%; Pred. No. 2e+06;  
 Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
 QY 1642 CGGCTGAGGAGTCCACACCCCTCAGAGCCGACCC 1679  
 Db 11 CTGCTGAGGCTGCCACACCCCTCTGCTGGGCCCCC 48  
 RESULT 6  
 AX248673 31 bp DNA PAT 28-SEP-2001  
 LOCUS  
 DEFINITION Sequence 752 from Patent WO0166800.  
 ACCESSION AX248673  
 VERSION AX248673.1 GI:15863296  
 KEYWORDS human.  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 REFERENCE 1 (bases 1 to 31)  
 AUTHORS Cargill, M., Ireland, J.S. and Lander, E.S.  
 TITLE Human single nucleotide polymorphisms  
 JOURNAL Patent: WO 0166800-A 752 13-SEP-2001;  
 WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)  
 FEATURES  
 source Location/Qualifiers  
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 /db\_xref="taxon:9606"  
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 Query Match 1..28 Score 21.6; DB 6; Length 31;  
 Best Local Similarity 80.0%; Pred. No. 2.6e+06;  
 Matches 24; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 979 GACCTCAAGCCCGCAGACCTCTCATCAAC 1008  
 Db 2 GACATCAAGCCCGCAGACCTCTCTGGTGGAC 31  
 RESULT 7  
 AX182243/c 42 bp DNA PAT 06-AUG-2001  
 LOCUS  
 DEFINITION Sequence 53 from Patent WO0142441.  
 ACCESSION AX182243  
 VERSION AX182243.1 GI:15133518  
 KEYWORDS  
 SOURCE synthetic construct.  
 ORGANISM  
 REDDY, S.I., Sathu, L.I., Shukla, V.C. and Ferralolo, G.I.  
 TITLE Placidal transformation

JOURNAL Patent: WO 0142441-A 53 14-JUN-2001;  
 International Centre for Genetic Engineering and Biotechnology (IT)  
 FEATURES  
 source Location/Qualifiers  
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 /organism="synthetic construct"  
 /db\_xref="taxon:32630"  
 /note="Primer"  
 BASE COUNT 15 a 10 c 11 g 6 t  
 ORIGIN  
 Query Match 1..28 Score 21.4; DB 6; Length 42;  
 Best Local Similarity 80.6%; Pred. No. 2.8e+06;  
 Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 270 ACCTGCTCTCTCTGGGAACTTCGTTCTGCA 300  
 Db 35 ACCTAGCGGCTCTCTGGGAACTTCGTTCTGCA 5  
 RESULT 8  
 AX382049/c 42 bp DNA PAT 18-MAR-2002  
 LOCUS  
 DEFINITION Sequence 53 from Patent WO0206497.  
 ACCESSION AX382049  
 VERSION AX382049.1 GI:19576871  
 KEYWORDS  
 SOURCE synthetic construct.  
 ORGANISM  
 REDDY, V.S. and Sathu, L.  
 TITLE Transplacental plants  
 JOURNAL Patent: WO 0206497-A 53 24-JAN-2002;  
 International Centre for Genetic Engineering and Biotechnology (IT)  
 FEATURES  
 source Location/Qualifiers  
 1..42  
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 /db\_xref="taxon:32630"  
 /note="Primer"  
 BASE COUNT 15 a 10 c 11 g 6 t  
 ORIGIN  
 Query Match 1..28 Score 21.4; DB 6; Length 42;  
 Best Local Similarity 80.6%; Pred. No. 2.8e+06;  
 Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 270 ACCTGCTCTCTCTGGGAACTTCGTTCTGCA 300  
 Db 35 ACCTAGCGGCTCTCTGGGAACTTCGTTCTGCA 5  
 RESULT 9  
 AR032544 46 bp DNA PAT 29-SEP-1999  
 LOCUS  
 DEFINITION Sequence 156 from patent US 5869241.  
 ACCESSION AR032544  
 VERSION AR032544.1 GI:5948149  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM  
 REDDY, S.I., Sathu, L.I., Shukla, V.C. and Ferralolo, G.I.  
 TITLE Placidal transformation



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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT      7 a      13 c      18 g      6 t      2 others
ORIGIN

Query Match      1.28; Score 21; DB 6; Length 46;
Best Local Similarity 71.1%; Pred. No. 3.5e+06;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Oy 550 AAGCCCTCAGCGCGCGCTCGTGTGCTGAGCTATC 587
      |||| |||| |||| |||| |||| |||| |||| ||||
Db 41 AAGCTCTCTGCAGCGCGCCGCGGCGGAGTGTCTATC 4

RESULT 15
A98791/c
LOCUS      A98791      46 bp      DNA      linear      PAT 26-JAN-2000
DEFINITION Sequence 24 from Patent WO9910358.
ACCESSION  A98791
VERSION    A98791.1 GI:6781812
KEYWORDS
SOURCE     unidentified.
ORGANISM   unidentified.
REFERENCE  1 (bases 1 to 46)
AUTHORS   Hegemann,P.
TITLE     METHOD FOR PRODUCING NUCLEIC ACID POLYMERS
JOURNAL   Patent: WO 9910358-A 24 04-MAR-1999;
          HEGEMANN PETER (DE)
FEATURES
          Location/Qualifiers
            source
              1..46
                /organism="unidentified"
                /db_xref="taxon:32644"
BASE COUNT      9 a      13 c      15 g      8 t
ORIGIN

Query Match      1.28; Score 20.8; DB 6; Length 46;
Best Local Similarity 78.1%; Pred. No. 3.9e+06;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 500 TCCCTGAGGGCTACCTGGAGAGCTGACCTC 531
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Db 37 TCCCGAGGGCTACCTGCAGGAGGCCACCATC 6

Search completed: March 4, 2003, 00:06:28
Job time : 4794 secs
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GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 3, 2003, 19:29:35 ; Search time 427 Seconds  
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Title: US-10-017-621-3

Perfect score: 1745

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Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /SID2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:\*
- 3: /SID2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:\*
- 4: /SID2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:\*
- 5: /SID2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:\*
- 6: /SID2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:\*
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- 8: /SID2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT:\*
- 9: /SID2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:\*
- 10: /SID2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT:\*
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- 12: /SID2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT:\*
- 13: /SID2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT:\*
- 14: /SID2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:\*
- 15: /SID2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT:\*
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- 18: /SID2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:\*
- 19: /SID2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:\*
- 20: /SID2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:\*
- 21: /SID2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:\*
- 22: /SID2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:\*
- 23: /SID2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:\*
- 24: /SID2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	ID	Description
C 1	24.8	1.4	50	22 AAL34335 Human SNP oligonuc
C 2	22.4	1.3	33	24 ABA04099 Human CDK5 related
C 3	22.4	1.3	33	24 ABA04100 Human CDK5 related
C 4	22	1.3	31	22 AAI30264 Human single nucle
C 5	22	1.3	50	22 AAI75639 Human single nucle
C 6	21.4	1.2	31	22 AAI29606 PCR primer SR53 fo
C 7	21.4	1.2	42	22 AAH22523 ifnc coding region
C 8	21.4	1.2	42	24 AAD29563 Human H1 histone 9
C 9	21.4	1.2	46	15 AAQ69406

10	21.4	1.2	45	18 AAT63868	Human H1 histone 9
11	21.4	1.2	46	20 AAX17156	Test sequence from
12	21.4	1.2	46	24 ABR84647	DNA binding molecu
13	21	1.2	21	22 AAH62195	PCTAIRE-1 polymorp
C 14	21	1.2	21	22 AAH70659	Human cervical can
C 15	21	1.2	50	22 AAL34286	Human SNP oligonuc
C 16	20.8	1.2	46	20 AAX22932	DE19736591 primer
C 17	20.6	1.2	45	16 AAT07598	RT-PCR primer/prob
C 18	20.6	1.2	45	16 AAT00670	Primer 143 for hum
C 19	20.6	1.2	50	22 AAT27875	Human SNP oligonuc
C 20	20.4	1.2	32	24 AAT72077	Xcds1 degenerate p
C 21	20.4	1.2	48	14 AAG50230	HIV pol. INS mutag
C 22	20.2	1.2	36	19 AAV46356	PCR primer for ser
C 23	20.2	1.2	40	16 AAT076190	Human 4-1BB 3' PCR
C 24	20.2	1.2	40	18 AAT91033	Human cytokine rec
C 25	20.2	1.2	40	24 ABL54053	Human proton-adeno
C 26	20.2	1.2	41	24 ABR48869	Human proton-adeno
C 27	20.2	1.2	41	24 ABR48870	Human prostate spe
C 28	20.2	1.2	45	22 AAD17287	Human A2b adenosin
C 29	20.2	1.2	49	20 AAZ31379	MUSIGHAEI Mouse Ig
C 30	20.2	1.2	50	19 AAV59127	Reverse PCR primer
C 31	20.2	1.2	50	22 AAS43538	Cornedoesmosin sin
C 32	20	1.1	41	19 AAV37843	CD4+ human T-lymph
C 33	20	1.1	41	24 AAL43819	Human large protei
C 34	20	1.1	46	21 AAZ91309	IL-6R and IL-6 fus
C 35	20	1.1	47	21 AAZ67885	Human map-related
C 36	20	1.1	50	22 AAL29783	Human SNP oligonuc
C 37	20	1.1	50	22 AAL34645	Human SNP oligonuc
C 38	19.8	1.1	46	21 AAC82589	Hammerhead ribozym
C 39	19.8	1.1	48	18 AAT76056	Human A2b adenosin
C 40	19.8	1.1	48	20 AAX53859	Human adenosine A2
C 41	19.8	1.1	48	21 AAF19424	Human adenosine A2
C 42	19.8	1.1	48	21 AAX33302	Low adenosine anti
C 43	19.8	1.1	48	21 AAO37074	Human adenosine A1
C 44	19.8	1.1	48	22 AAH74232	Nucleotide sequenc
C 45	19.6	1.1	31	22 AAI30029	Human single nucle

#### ALIGNMENTS

RESULT 1

AAL34335/C

ID AAL34335 standard; DNA; 50 BP.

XX AAL34335;

AC AAL34335;

DT 24-JAN-2002 (first entry)

DE Human SNP oligonucleotide #7343.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 XX neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;  
 XX ankyloid protein; angiotensin; apoptosis related protein; cadherin;  
 XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 XX complement related protein; cytochrome; kinesin; cytokine; interferon;  
 XX interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 XX multifactorial disease; autoimmune disease; infection;  
 XX nervous system disease; ss.

OS Homo sapiens.

PN WO200147944-A2.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US35498.

XX 28-DEC-1999; 99US-0173419.

XX 27-DEC-2000; 2000US-0173419.

XX (CURA-) CURAGEN CORP.

PI Shimkets RA, Leach M;  
 DR WPI; 2001-465210/50.  
 XX  
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g.  
 PT cancer, autoimmune diseases and infections  
 XX  
 PS Claim 1; Page 3563; 4143pp; English.  
 XX  
 CC The present invention relates to oligonucleotides encoding polymorphic  
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
 CC histones, kinases, colony stimulating factors, complement related  
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,  
 CC G-protein coupled receptors and thioesterases. The present sequence is  
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded  
 CC by them may be used in the prevention, diagnosis and treatment of  
 CC diseases associated with inappropriate expression of the proteins listed  
 CC above. Disorders that may be prevented, diagnosed and/or treated include  
 CC multifactorial diseases with a genetic component, such as autoimmune  
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
 CC leukaemia), diseases of the nervous system and an infection of pathogenic  
 CC organisms.  
 XX  
 SQ Sequence 50 BP; 7 A; 13 C; 14 G; 16 T; 0 Other;  
 Query Match 1.4%; Score 24.8; DB 22; Length 50;  
 Best Local Similarity 72.7%; Pred. No. 7.8e+03;  
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
 OY 1619 CAGACCGAGGCCCGCAGCAGCGCGGTGGAGGATGCCACAC 1662  
 DB 45 CAGACCGAGGCCCGCAGCAGCTCATCTGCGAGATTATGCACAC 2  
 RESULT 2  
 ABA04099  
 ID ABA04099 standard; DNA; 33 BP.  
 XX  
 AC ABA04099;  
 XX  
 DT 21-FEB-2002 (first entry)  
 XX  
 DE Human Cdk5 related PCR primer SEQ ID NO:18.  
 XX  
 KW Human; beta-amyloid; cyclin-dependent kinase inhibitor; nerve cell;  
 KW amyloid precursor protein; APP; Cdk5; PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200182967-A1.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PP 25-APR-2001; 2001WO-JP03555.  
 XX  
 PR 28-APR-2000; 2000JP-0131037.  
 XX  
 PA (YAMA) YAMANOUCHI PHARM CO LTD.  
 XX  
 PA (SUZU) SUZUKI T.  
 XX  
 PI Suzuki T, Watanabe T, Kawabata S, Hachiya S;  
 XX  
 DR WPI; 2002-026209/03.  
 XX  
 PT Medicinal compositions for the treatment of dementia and Alzheimer's  
 PT disease, comprise compounds that suppress beta amyloid production  
 XX  
 PS Example 6; Page 23; 62pp; Japanese.  
 XX

CC The present invention describes medicinal compositions (I) inhibiting  
 CC beta-amyloid production comprising an active component a substance that  
 CC inhibits the activity of cyclin-dependent kinase (CDK). Also described  
 CC are: (1) a method for screening compounds for their ability to inhibit  
 CC the production of beta-amyloid by contacting with beta-amyloid producing  
 CC cells; and (2) screening kits. (I) have neurotropic and neuroprotective  
 CC activities. (I) suppress the phosphorylation of amyloid precursor protein  
 CC (APP) which is an essential step in the production of beta-amyloid. (I)  
 CC can be used in the treatment and prevention of neurodegenerative diseases  
 CC such as dementia and Alzheimer's disease. The present sequence represents  
 CC a PCR primer which is used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 33 BP; 6 A; 6 C; 11 G; 10 T; 0 other;  
 Query Match 1.3%; Score 22.4; DB 24; Length 33;  
 Best Local Similarity 81.2%; Pred. No. 2.8e+04;  
 Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 OY 1018 GAGCTCAAGCTGGCTGACTTTGGCTGGCCG 1049  
 DB 2 GAGCTGAATTTGGCTAATTTGGCTGGCTCG 33  
 RESULT 3  
 ABA04100/c  
 ID ABA04100 standard; DNA; 33 BP.  
 XX  
 AC ABA04100;  
 XX  
 DT 21-FEB-2002 (first entry)  
 XX  
 DE Human Cdk5 related PCR primer SEQ ID NO:19.  
 XX  
 KW Human; beta-amyloid; cyclin-dependent kinase inhibitor; nerve cell;  
 KW amyloid precursor protein; APP; Cdk5; PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200182967-A1.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PP 25-APR-2001; 2001WO-JP03555.  
 XX  
 PR 28-APR-2000; 2000JP-0131037.  
 XX  
 PA (YAMA) YAMANOUCHI PHARM CO LTD.  
 XX  
 PA (SUZU) SUZUKI T.  
 XX  
 PI Suzuki T, Watanabe T, Kawabata S, Hachiya S;  
 XX  
 DR WPI; 2002-026209/03.  
 XX  
 PT Medicinal compositions for the treatment of dementia and Alzheimer's  
 PT disease, comprise compounds that suppress beta amyloid production  
 XX  
 PS Example 6; Page 23; 62pp; Japanese.  
 XX  
 CC The present invention describes medicinal compositions (I) inhibiting  
 CC beta-amyloid production comprising an active component a substance that  
 CC inhibits the activity of cyclin-dependent kinase (CDK). Also described  
 CC are: (1) a method for screening compounds for their ability to inhibit  
 CC the production of beta-amyloid by contacting with beta-amyloid producing  
 CC cells; and (2) screening kits. (I) have neurotropic and neuroprotective  
 CC activities. (I) suppress the phosphorylation of amyloid precursor protein  
 CC (APP) which is an essential step in the production of beta-amyloid. (I)  
 CC can be used in the treatment and prevention of neurodegenerative diseases  
 CC such as dementia and Alzheimer's disease. The present sequence represents  
 CC a PCR primer which is used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 33 BP; 10 A; 11 C; 6 G; 6 T; 0 other;





```

DT 18-OCT-2001 (first entry)
XX Human single nucleotide polymorphism (SNP) PCTAIRE3 1.
DB Human; resequence; genotype; disease; forensic; paternity testing;
XX single nucleotide polymorphism; SNP; ss.
RW Homo sapiens.
XX Key Location/Qualifiers
FH Variation replace(16.C)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN WO200156800-A2.
XX 13-SEP-2001.
XX
XX 07-NAR-2001; 2001WO-US07268.
XX
XX 07-MAR-2000; 2000US-0187510.
XX 22-MAY-2000; 2000US-0206129.
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX Cargill M, Ireland JS, Lander ES;
XX NPI; 2001-522952/57.
XX
XX Nucleic acid molecules from the human genome which include polymorphic
XX sites, useful in methods for predicting the presence, absence or
XX severity of a particular phenotype or disorder (e.g. diabetes)
XX associated with a particular genotype -
XX
XX Claim 1; Page 34; 145pp; English.
XX
XX The invention relates to the identification of nucleic acid molecules
XX (AA129513-AA13114) from the human genome which include polymorphic sites
XX which can predispose individuals to disease. Various genes from a number
XX of individuals were resequenced and single nucleotide polymorphisms
XX (SNPs) in these genes discovered. The method is useful for predicting the
XX presence, absence or severity of a particular phenotype or disorder (e.g.
XX diabetes) associated with a particular genotype. The nucleic acids
XX containing the polymorphic sites may be useful in forensics and paternity
XX testing.
XX
XX Sequence 31 BP; 6 A; 9 C; 8 G; 8 T; 0 other;
SQ
Query Match 1.2%; Score 21.4; DB 22; Length 31;
Best Local Similarity 80.6%; Pred. No. 4.9e+04;
Matches 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 577 GTCAGCCTATCTGAGATTGCTTGGGAAC 607
Db 1 GCCTCCCTGTCAGACATTGCTTGGGAAC 31
RESULT 7
AAH22523/c
ID AAH22523 standard; DNA; 42 BP.
XX
XX AAH22523;
XX
XX 22-AUG-2001 (first entry)
XX
XX PCR primer SR53 for amplifying a 1fng coding region.
XX
XX Transplastome; plastome; plastid; chloroplast; transgene; plant;
XX 1fng; PCR primer; ss.
XX
XX Synthetic.
XX
XX WO200142441-A2.
XX

```

```

XX
PD 14-JUN-2001.
XX
XX 08-DEC-2000; 2000WO-EP12446.
XX
XX 08-DEC-1999; 99GB-0029075.
XX 14-JUL-2000; 2000GB-0017369.
XX
XX (ITGE-) INT CENT GENETIC ENG & BIOTECHNOLOGY.
XX Reddy S, Sadhu L, Shukla V, Ferraiolo G;
XX WPT; 2001-381671/40.
XX
XX Obtaining a stable transplastome for producing a transplastomic cell,
XX plant or seed, comprises transforming a recipient plastome with a
XX polynucleotide comprising a 5' and 3' sequence homologous to the
XX recipient -
XX
XX Example 12; Page 127; 128pp; English.
XX
XX The invention relates to a method of obtaining a stable transplastome,
XX by transforming a recipient plastome (RP) with a polynucleotide having a
XX 5' sequence homologous to a region of RP, and joined to it a sequence
XX heterologous to RP comprising a coding region operably linked to
XX regulatory region capable of securing expression of coding region in the
XX plastid and joined to it, and a 3' sequence homologous to a region of RP.
XX The method is useful for obtaining a transplastomic plastid, by
XX transforming a plastome within a plastid such as proplastid, amyloplast,
XX chromoplast, etioplast or leucoplast, preferably chloroplast. The method
XX is useful for obtaining a transplastomically expressed protein. The
XX method provides high, uniform, reliable expression of transgenes in
XX plants, with stable inheritance of the trait by avoiding the potential
XX for the dangerous spread of transgenes to the ecosystem. The present
XX sequence represents a PCR primer for amplifying a 1fng coding region,
XX used in generating expression vectors for 1fng in chloroplasts.
XX
XX Sequence 42 BP; 15 A; 10 C; 11 G; 6 T; 0 other;
SQ
Query Match 1.2%; Score 21.4; DB 22; Length 42;
Best Local Similarity 80.6%; Pred. No. 5.6e+04;
Matches 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 270 ACGTGCTGCTCCTGGGAACTTCGTTCTGCA 300
Db 35 ACGTACGGGTCTCTGGCGACCTTCGATCTGCA 5
RESULT 8
AAD29563/c
ID AAD29563 standard; DNA; 42 BP.
XX
XX AAD29563;
XX
XX 07-MAY-2002 (first entry)
XX
XX 1fng coding region DNA amplifying PCR primer, SR53.
XX
XX Transgenic plant; transplastomic plant; medicament; PCR primer; ss.
XX
XX Unidentified.
XX
XX WO200206497-A2.
XX
XX 24-JAN-2002.
XX
XX 13-JUL-2001; 2001WO-EP08132.
XX
XX 14-JUL-2000; 2000GB-0017397.
XX
XX (ITGE-) INT CENT GENETIC ENG & BIOTECHNOLOGY.
XX Reddy VS, Sadhu L;
XX

```



Claim 6; Column 177-178; 264pp; English.

PS The sequences given in AAT63713-4312 represent duplex DNA's which act  
 CC as target regions in the method of the invention. The method for  
 CC altering the binding characteristics of a DNA-binding protein to duplex  
 CC DNA comprises contacting the duplex DNA with a small molecule which  
 CC binds sequence-specifically to a target region, where, when the small  
 CC molecule is bound to the target region, it is adjacent to, but not  
 CC overlapping by more than 4 bp, a binding site for a DNA-binding protein.  
 CC The small molecule is added at a concentration effective to alter the  
 CC binding of the DNA binding protein, pref. TFID, to its binding site on  
 CC the duplex DNA. The binding of the small molecule may inhibit or  
 CC enhance the binding of the DNA-binding protein to its binding site. The  
 CC compounds isolated using this method are potentially useful as  
 CC therapeutic agents for treatment of any disease which involves a  
 CC specific DNA sequence, e.g. cancer, or inherited genetic disorders etc.  
 CC The method is suitable for screening large biological or chemical  
 CC libraries and allows determination of sequence-specific and relative  
 CC affinities of known DNA-binding agents for different DNA sequences.  
 CC The design of these duplex DNA's allows a single DNA:protein interaction  
 CC to be used for screening sequence-specific, or preferential, DNA binding  
 CC proteins that recognise almost any possible sequence (see also AAT49539-  
 CC 74).

Sequence 46 BP; 9 A; 14 C; 16 G; 7 T; 0 other;

Query Match 1.2%; Score 21.4; DB 18; Length 46;

Best Local Similarity 71.8%; Pred. No. 5.8e+04;

Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 1641 GCGGCTGGAGGATGCGACACCCCTCACAGGCGAGCCGCC 1679

IIII I IIII IIII IIII IIII IIII IIII IIII

DB 2 GCGGTGGATTGGAGCGCTCCACCAATCACAGGCGAGCCGCC 40

RESULT 11

AA17156

ID AAX17156 standard; DNA: 46 BP.

XX AAX17156;

AC AAX17156;

XX AAX17156;

DT 05-MAY-1999 (first entry)

DE Test sequence from human H1 histone gene FNC16.

XX Test sequence; DNA-binding molecule; screening sequence; human;

KW nucleic acid amplification; target; viral; ds.

XX Homo sapiens.

OS US5869241-A.

XX US5869241-A.

PN 09-FEB-1999.

XX 09-FEB-1999.

PD 07-JUN-1995; 9505-0475228.

XX 07-JUN-1995; 9505-0475228.

PF 20-DEC-1993; 9305-0171389.

XX 20-DEC-1993; 9305-0171389.

PR 27-JUN-1991; 91US-0723618.

XX 27-JUN-1991; 91US-0723618.

PR 23-DEC-1992; 92US-0996783.

XX 23-DEC-1992; 92US-0996783.

PR 17-SEP-1993; 93US-0123936.

XX 17-SEP-1993; 93US-0123936.

PR 07-JUN-1995; 9505-0475228.

XX 07-JUN-1995; 9505-0475228.

PA (GENE-) GENELABS TECHNOLOGIES INC.

XX (GENE-) GENELABS TECHNOLOGIES INC.

PI Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;

XX WPI; 1999-152755/13.

DR WPI; 1999-152755/13.

XX Determination of DNA sequence preference of a DNA-binding molecule -

PT based on inhibition of binding of protein to oligonucleotide

PT sequence attached to test sequence

XX Claim 3; Columns 179-180; 270pp; English.

PS Claim 3; Columns 179-180; 270pp; English.

XX Sequences AAX17001 to AAX17600 represent specifically claimed target  
 CC test sequences that are used in the method of the invention of  
 CC determining the DNA sequence preference of a DNA-binding molecule. The  
 CC method comprises: (i) adding a test molecule and a DNA-binding protein to  
 CC a mixture of duplex DNA test oligonucleotides, each of the test  
 CC oligonucleotides having a test sequence adjacent to a screening sequence,  
 CC where the screening sequence binds to the DNA-binding protein with a  
 CC binding affinity that is independent of the DNA sequence of the test  
 CC sequence, and where the mixture of duplex DNA test oligonucleotides  
 CC includes several test sequences; (ii) incubating the test molecule, the  
 CC mixture of duplex DNA test oligonucleotides and the DNA-binding protein  
 CC for a time sufficient to permit binding of the test molecule to test  
 CC sequences in the duplex DNA; (iii) separating unbound test  
 CC oligonucleotides from test oligonucleotides bound to binding protein;  
 CC (iv) amplifying the unbound test oligonucleotides; (v) repeating steps  
 CC (ii) to (iv); (vi) isolating the amplified test oligonucleotides; and  
 CC (vii) sequencing the isolated test oligonucleotides. Test sequences  
 CC AAX17001-X17481 and AAX17600 correspond to promoter targets for human  
 CC genes and test sequences AAX17482-X17599 correspond to promoter targets  
 CC for viral genes.

Sequence 46 BP; 9 A; 14 C; 16 G; 7 T; 0 other;

Query Match 1.2%; Score 21.4; DB 20; Length 46;

Best Local Similarity 71.8%; Pred. No. 5.8e+04;

Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 1641 GCGGCTGGAGGATGCGACACCCCTCACAGGCGAGCCGCC 1679

IIII I IIII IIII IIII IIII IIII IIII IIII

DB 2 GCGGTGGATTGGAGCGCTCCACCAATCACAGGCGAGCCGCC 40

RESULT 12

ABK82647

ID ABK82647 standard; DNA: 46 BP.

XX ABK82647;

AC ABK82647;

XX ABK82647;

DT 27-AUG-2002 (first entry)

XX DNA binding molecule screening method test sequence #156.

DE DNA binding molecule screening; inhibition of transcription;

XX infection; human immunodeficiency virus; HIV; parasite; cancer;

KW cardiovascular; respiratory; gastrointestinal; endocrine; metabolic;

XX rheumatic; immunological; haematological; neurological;

KW psychiatric; dermatological; ophthalmological; musculo-skeletal;

XX urogenital disorder; ss.

XX Synthetic.

OS US5384208-B1.

XX US5384208-B1.

PN 07-MAY-2002.

XX 07-MAY-2002.

PD 15-JUL-1999; 99US-0354947.

XX 15-JUL-1999; 99US-0354947.

PF 20-DEC-1993; 93US-0171389.

XX 20-DEC-1993; 93US-0171389.

PR 07-JUN-1995; 95US-0482080.

XX 07-JUN-1995; 95US-0482080.

PR 27-JUN-1991; 91US-0723618.

XX 27-JUN-1991; 91US-0723618.

PR 23-DEC-1992; 92US-0996783.

XX 23-DEC-1992; 92US-0996783.

PR 17-SEP-1993; 93US-0123936.

XX 17-SEP-1993; 93US-0123936.

PA (GENE-) GENELABS TECHNOLOGIES INC.

XX (GENE-) GENELABS TECHNOLOGIES INC.

PI Edwards CA, Cantor CR, Andrews BM, Turin LM, Fry KE;

XX WPI; 2002-442819/47.

DR WPI; 2002-442819/47.

XX Decreasing transcriptional activity of genes for treating infections or

PT cancer; by administration of an agent that binds to two non-overlapping

XX regions of the gene

PT regions of the gene







DB 2 GGAGCAATCCACCACCTGGGTGGCTCCCACTCTCTCTCTCTG 44

## RESULT 2

PCT-US95-13830-5

: Sequence 5, Application PC/TUS9513830

: GENERAL INFORMATION:

: APPLICANT: Genentech, Inc.

: APPLICANT: New England Deaconess Hospital Corp.

: TITLE OF INVENTION: Methods and Kits Using Macrophage Stimulating

: PROTEIN

: NUMBER OF SEQUENCES: 10

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Genentech, Inc.

: STREET: 460 Point San Bruno Blvd

: CITY: South San Francisco

: STATE: California

: COUNTRY: USA

: ZIP: 94080

: COMPUTER READABLE FORM:

: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: WinPatIn (Genentech)

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: PCT/US95/13830

: FILING DATE:

: CLASSIFICATION:

: ATTORNEY/AGENT INFORMATION:

: NAME: Marschang, Diane L.

: REGISTRATION NUMBER: 35,600

: REFERENCE/DOCKET NUMBER: P0912PCT

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: 415/225-5416

: TELEFAX: 415/952-9881

: TELEX: 910/371-7168

: INFORMATION FOR SEQ ID NO: 5:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 47 base pairs

: TYPE: Nucleic Acid

: STRANDEDNESS: Single

: TOPOLOGY: Linear

: PCT-US95-13830-5

Query Match 1.34; Score 22.2; DB 5; Length 47;

Best Local Similarity 69.84; Pred. No. 5.8e+03;

Matches 30; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 241 GGCGGAGTGGACCTGGAGAGGCCCCACACGCTGCTCTCTG 283

DB 2 GGAGCAATCCACCACCTGGGTGGCTCCCACTCTCTCTCTG 44

## RESULT 3

US-08-507-426C-9/c

: Sequence 9, Application US/08507426C

: Patent No. 6265634

: GENERAL INFORMATION:

: APPLICANT: Lenexa, Philippe

: TITLE OF INVENTION: POLYRIBOZYME CAPABLE OF CONFERRING ON PLANTS RESISTANCE

: TO VIRUSES AND RESISTANT PLANTS PRODUCING THIS

: POLYRIBOZYME

: FILE REFERENCE: 43944-A-PCT-US

: CURRENT APPLICATION NUMBER: US/08/507,426C

: CURRENT FILING DATE: 1995-10-25

: PRIOR FILING DATE: 1995-10-25

: PRIOR APPLICATION NUMBER: 43944-A-PCT-US

: NUMBER OF SEQ ID NOS: 14

: SOFTWARE: Patent In Ver. 2.1

: SEQ ID NO 9

: LENGTH: 44

: TYPE: DNA

: ORGANISM: Artificial Sequence

: FEATURE:  
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
: OTHER INFORMATION: ribozymes and portions thereof  
: US-08-507-426C-9

Query Match 1.28; Score 21.8; DB 4; Length 44;

Best Local Similarity 70.74; Pred. No. 7.2e+03;

Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1559 CCGTCATGCTGACCTCAGGCGACGACCTTCGCGTGGTG 1599

DB 42 CTTGTGGACGACTCAGGCGACCTCTCTTGGCGCTGCTG 2

## RESULT 4

US-08-171-389-156

: Sequence 156, Application US/08171389

: Patent No. 5578444

: GENERAL INFORMATION:

: APPLICANT: Edwards, Cynthia A.

: APPLICANT: Cantor, Charles R.

: APPLICANT: Andrews, Beth M.

: APPLICANT: Turin, Lisa M.

: APPLICANT: Fiy, Kirk E.

: TITLE OF INVENTION: Sequence-Directed DNA Binding

: MOLECULES, COMPOSITIONS AND METHODS

: NUMBER OF SEQUENCES: 641

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Genelabs Technologies, Inc.

: STREET: 505 Penobscot Drive

: CITY: Redwood City

: STATE: CA

: COUNTRY: USA

: ZIP: 94063

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: Patent In Release #1.0, Version #1.25

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/08/171,389

: FILING DATE:

: CLASSIFICATION: 435

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: US 08/123,936

: FILING DATE: 17-SEP-1993

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: US 07/995,783

: FILING DATE: 23-DEC-1992

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: US 07/723,618

: FILING DATE: 27-JUN-1991

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: US 08/081,070

: FILING DATE: 22-JUN-1993

: ATTORNEY/AGENT INFORMATION:

: NAME: Fabiad, Gary R.

: REGISTRATION NUMBER: 33,875

: REFERENCE/DOCKET NUMBER: 4600-0175/G19P3

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: (415) 324-0880

: TELEFAX: (415) 324-0960

: INFORMATION FOR SEQ ID NO: 156:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 46 base pairs

: TYPE: nucleic acid

: STRANDEDNESS: double

: TOPOLOGY: linear

: MOLECULE TYPE: DNA (genomic)

: HYPOTHETICAL: NO

: ORIGINAL SOURCE:

: INDIVIDUAL ISOLATE: Human H1 histone gene FNC16

: US-08-171-389-156







```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Pencabot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12388
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175.41/G19PCT2
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 156:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human H1 histone gene FNC16
PCT-US93-12388-156

Query Match 1.2%: Score 21.4; DB 5; Length 46;
Best Local Similarity 71.8%; Pred. No. 9.1e+03;
Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 1641 CGCGCTGAGGGTGCACACCCCTCACAGGCGAGCC 1679
||||| 1 |||| 11 |||| ||||| |||||
DB 2 CGCGTGGATTGGACGCTCCACCAATCACAGGCGAGCC 40

RESULT 10
US-08-233-009-33
Sequence 33, Application US/08233009
Patent No. 5646156
GENERAL INFORMATION:
APPLICANT: Jacobson, Marlene A
APPLICANT: Johnson, Robert G
APPLICANT: Salvatore, Christopher A
TITLE OF INVENTION: INHIBITION OF EOSINOPHIL
TITLE OF INVENTION: ACTIVATION THROUGH A3 ADENOSINE RECEPTOR ANTAGONISM
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: United States
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Pencabot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,009
FILING DATE: 23-APR-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: 19219
TELEPHONE: (908) 594-3901
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-233-009-33

Query Match 1.2%: Score 20.6; DB 1; Length 45;
Best Local Similarity 67.4%; Pred. No. 1.5e+04;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 737 CCTGCACCGCCATCGGGAGGTGCTCCTGCTCAAGGACCTCAA 779
|||||| 111 1 11 ||||| ||||| 11 1
DB 2 CCTGCACCGCCACTGCTTAGCCCCCTCGCCAGGCTCATCCA 44

RESULT 11
US-08-285-936-38/c
Sequence 38, Application US/08285936
Patent No. 5728821
GENERAL INFORMATION:
APPLICANT: Yelton, Dale
APPLICANT: Glaser, Scott
APPLICANT: Huse, William
APPLICANT: Rosok, Mae J.
TITLE OF INVENTION: No. 5728821el Mutant BR96 Antibodies and
TITLE OF INVENTION: Functional Equivalents Reactive With Human Carcinomas
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90025-3395
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/285,936
FILING DATE: 04-AUG-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436.16US01
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/050,478  
FILING DATE: 26-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/02908  
FILING DATE: 29-MAR-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/858,747  
FILING DATE: 27-MAR-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MORRY, MARY J.  
REGISTRATION NUMBER: 34,398  
REFERENCE/DOCKET NUMBER: 2026-4006US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)758-4800  
TELEFAX: (212)751-6849  
INFORMATION FOR SEQ ID NO: 47:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 BASE PAIRS  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
US-08-050-478-47

Query Match 1.2%; Score 20.4; DB 2; Length 48;  
Best Local Similarity 71.1%; Pred. No. 1.7e+04;  
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
Qy 325 GAGATTGTGCACGAGGACTTGAAGATGGGGTCTGATGG 362  
||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 7 GACACGGTGCCTGCTGAAGTTGAAGCGGGGATGGATGG 44

RESULT 15  
US-09-414-117-47  
Sequence 47, Application US/09414117  
Patent No. 6291884  
GENERAL INFORMATION:  
APPLICANT:  
APPLICANT:  
TITLE OF INVENTION: METHOD OF ELIMINATING  
NUMBER OF INVENTION: INHIBITORY/INSTABILITY REGIONS OF mRNA  
NUMBER OF SEQUENCES: 130  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/414,117  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/850,049  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/02908

FILING DATE: 29-MAR-1993  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/858,747  
FILING DATE: 27-MAR-1992  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MORRY, MARY J.  
REGISTRATION NUMBER: 34,398  
REFERENCE/DOCKET NUMBER: 2026-4006US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)758-4800  
TELEFAX: (212)751-6849  
INFORMATION FOR SEQ ID NO: 47:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 BASE PAIRS  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
US-09-414-117-47  
Query Match 1.2%; Score 20.4; DB 4; Length 48;  
Best Local Similarity 71.1%; Pred. No. 1.7e+04;  
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
Qy 325 GAGATTGTGCACGAGGACTTGAAGATGGGGTCTGATGG 362  
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Db 7 GACACGGTGCCTGCTGAAGTTGAAGCGGGGATGGATGG 44  
Search completed: March 4, 2003, 00:52:00  
Job time: 80 secs

GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 3, 2003, 22:39:05 ; Search time 133 Seconds  
(without alignments)  
8182.066 Million cell updates/sec

Title: US-10-017-621-3

Perfect score: 1745

Sequence: 1 tgaacacgcglaagatg.....gtcacctgccttcttcc 1745

Scoring table: IDENTITY\_NUC

Gapop 10.0 ; Gapext 1.0

Searched: 460893 seqs, 311809382 residues

Total number of hits satisfying chosen parameters: 254638

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

#### Database :

Published Applications NA:

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/CT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/CTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	21.8	1.2	48	9	US-10-054-444-6
2	21.6	1.2	31	10	US-09-801-274-752
3	21.4	1.2	45	9	US-10-029-413A-25
4	21	1.2	31	10	US-09-801-274-94
5	20.4	1.2	48	9	US-09-943-722-47
6	20	1.1	45	10	US-09-147-142-11
7	20	1.1	45	10	US-09-147-142-12
8	19.8	1.1	40	10	US-09-263-959-758
9	19.6	1.1	42	10	US-09-790-417-235
10	19.4	1.1	45	12	US-10-073-256-27
11	19.4	1.1	45	12	US-10-073-256-35
12	19.2	1.1	31	10	US-09-801-274-517
13	19.2	1.1	46	10	US-09-263-959-121
14	19	1.1	43	9	US-09-376-940-23
15	19	1.1	45	10	US-09-818-056-32
16	18.8	1.1	47	9	US-10-118-231-9
17	18.8	1.1	48	9	US-09-840-277-104
18	18.8	1.1	48	9	US-09-840-277-105
19	18.8	1.1	48	10	US-09-753-436-67

c	20	18.8	1.1	49	9	US-09-840-277-107	Sequence 107, App
	21	18.6	1.1	25	10	US-09-866-108-15295	Sequence 15295, A
	22	18.6	1.1	48	9	US-09-864-785-3433	Sequence 3433, Ap
	23	18.4	1.1	41	9	US-09-938-842A-5256	Sequence 5256, Ap
	24	18.4	1.1	48	10	US-09-781-534A-18	Sequence 18, Appl
	25	18.2	1.0	36	9	US-10-213-248-31	Sequence 31, Appl
	26	18.2	1.0	36	10	US-10-213-247-31	Sequence 31, Appl
	27	18.2	1.0	36	10	US-09-855-722-31	Sequence 31, Appl
	28	18.2	1.0	50	9	US-09-943-722-9	Sequence 9, Appl
c	29	18	1.0	42	10	US-09-790-417-233	Sequence 233, App
	30	18	1.0	43	12	US-10-043-142-4	Sequence 4, Appl
	31	18	1.0	46	9	US-10-026-914-8	Sequence 8, Appl
	32	18	1.0	46	9	US-10-026-914-10	Sequence 10, Appl
	33	18	1.0	46	9	US-10-026-914-14	Sequence 14, Appl
	34	18	1.0	46	9	US-10-026-914-16	Sequence 16, Appl
	35	18	1.0	48	9	US-09-864-785-3226	Sequence 3226, Ap
c	36	17.8	1.0	35	9	US-10-051-989-2	Sequence 2, Appl
	37	17.8	1.0	35	9	US-09-861-097-2	Sequence 25, Appl
	38	17.8	1.0	42	10	US-09-865-807-25	Sequence 24, Appl
	39	17.8	1.0	45	12	US-10-073-256-24	Sequence 25, Appl
	40	17.8	1.0	45	12	US-10-073-256-25	Sequence 33, Appl
c	41	17.8	1.0	45	12	US-10-073-256-33	Sequence 34, Appl
	42	17.8	1.0	45	12	US-10-073-256-34	Sequence 3267, Ap
	43	17.8	1.0	48	9	US-09-864-785-3311	Sequence 3311, Ap
	44	17.8	1.0	48	9	US-09-864-785-3311	Sequence 3491, Ap
	45	17.8	1.0	48	9	US-09-864-785-3491	

#### ALIGNMENTS

#### RESULT 1

US-10-054-444-6

; Sequence 6, Application US/10054444

; Patent No. US20020154342A1

; GENERAL INFORMATION:

; APPLICANT: Guyre, Paul M.

; APPLICANT: Goldstein, Joel

; APPLICANT: Wu, Zining

; APPLICANT: Sun, Wanwen

; TITLE OF INVENTION: Recombinant Cat Allergen, Fel d1, Expressed in Baculovirus for Diagnosis and Treatment of Cat Allergy

; FILE REFERENCE: DC-0118

; CURRENT APPLICATION NUMBER: US/10/054.444

; PRIOR FILING DATE: 2002-01-22

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/410.963

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 5

; LENGTH: 48

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-054-444-6

Query Match

Best Local Similarity

Matches

Score 21.8; DB 9; Length 48;

Conservative

0; Mismatches 12; Indels 0; Caps 0;

#### RESULT 2

US-09-801-274-752

; Sequence 752, Application US/09801274

; Patent No. US20020032319A1

; GENERAL INFORMATION:

; APPLICANT: Cargill, Michele

; APPLICANT: Ireland, James S.

RESULT 4  
US-09-801-274-94  
; Sequence 94, Application US/09801274  
; Patent No. US20020032319A1  
; GENERAL INFORMATION:  
; APPLICANT: Cargill, Michele  
; APPLICANT: Ireland, James S.  
; APPLICANT: Lauder, Eric S.  
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS  
; FILE REFERENCE: 2825.2009-001  
; CURRENT APPLICATION NUMBER: US/09/801.274  
; CURRENT FILING DATE: 2001-03-07  
; PRIOR APPLICATION NUMBER: US 60/187.510  
; PRIOR FILING DATE: 2000-03-07

SEQUENCE CHARACTERISTICS:  
LENGTH: 48 BASE PAIRS  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE

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;
; TOPOLOGY: LINEAR
; US-09-943-722-47
;
; Query Match 1.1%; Score 20.4; DB 9; Length 48;
; Best Local Similarity 71.1%; Pred. No. 2.3e+04;
; Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
;
; QY 325 GAGATGTCGACGAGGACTGAGATGGGGTCTGATGG 352
;      ||||| ||||| ||||| ||||| ||||| |||||
; DB 7 GAGACGGTCCCGTGAAGTTGAAGCCGGGATGGATGG 44
;
; RESULT 6
; US-09-147-142-11
; Sequence 11, Application US/09147142
; Patent No. US20020018749A1
; GENERAL INFORMATION:
; APPLICANT: HUDSON, Peter John
; APPLICANT: KORTT, Alex Andrew
; APPLICANT: IRVING, Robert Alexander
; APPLICANT: ATWELL, John Leslie
; TITLE OF INVENTION: HIGH AVIDITY POLYVALENT AND POLYSPECIFIC REAGENTS
; FILE REFERENCE: 016786/0212
; CURRENT APPLICATION NUMBER: US/09/147.142
; CURRENT FILING DATE: 1999-03-05
; EARLIER APPLICATION NUMBER: PCT/AU98/00212
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: AU PO 5917
; EARLIER FILING DATE: 1997-03-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
;
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: Oligonucleotide used to insert codon between VH
; OTHER INFORMATION: and VL domains of NC10 scFv-0
; US-09-147-142-11
;
; Query Match 1.1%; Score 20; DB 10; Length 45;
; Best Local Similarity 65.9%; Pred. No. 2.8e+04;
; Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
;
; QY 643 GGTACTATGCCACCGTCTACAAAGGCAAAAGCAAGCTCACAGA 586
;      || ||| || ||||| || ||| || ||||| || ||| || ||||| ||
; DB 45 GGGACCACGGTCACCGTCTCCGGTGGTGATATCGAGCTCACACA 2
;
; RESULT 8
; US-09-263-959-758
; Sequence 758, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: HOOD, Leroy E.
; APPLICANT: ROVEN, Lee
; APPLICANT: KOOP, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH U
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263.959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 758:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-263-959-758
;
; Query Match 1.1%; Score 19.8; DB 10; Length 40;
; Best Local Similarity 77.4%; Pred. No. 3e+04;
; Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
;
; QY 1689 CTTCCCTGCTTACTCTCTGCTGCTACCTGCTG 1719
;      || ||||| || ||||| || ||||| || ||||| || ||||| ||
; DB 3 CTTCCCTTTCTCTCTCTCTCTCTCTCTCTGCTG 33
;
; RESULT 9
; US-09-790-417-235/c
; Sequence 235, Application US/09790417
; Patent No. US20010031470A1
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W
; APPLICANT: Lewis, Martin K.
; APPLICANT: Lleppe, Donna
```



**TITLE OF INVENTION: System and Method for Tracking and Controlling Infections**

MEDIA LIFE: floppy disk  
COMPUTER: IBM PC compatible



GenCore version 5.1.4\_P5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 3, 2003, 22:34:05 ; Search time 2628 seconds  
(without alignments)  
10753.853 Million cell updates/sec

Title: US-10-017-621-3  
Perfect score: 1745  
Sequence: 1 tgsaagcagcgtaaaggatg.....gtccactgcccactgtcc 1745

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 100%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST.\*

- 1: em\_estba.\*
- 2: em\_esthum.\*
- 3: em\_estlin.\*
- 4: em\_estm.\*
- 5: em\_estov.\*
- 6: em\_estpl.\*
- 7: em\_estro.\*
- 8: em\_hc.\*
- 9: gb\_estl.\*
- 10: gb\_est2.\*
- 11: gb\_hc.\*
- 12: gb\_est3.\*
- 13: gb\_est4.\*
- 14: gb\_est5.\*
- 15: em\_estfun.\*
- 16: em\_estom.\*
- 17: gb\_gss.\*
- 18: em\_gss\_hum.\*
- 19: em\_gss\_inv.\*
- 20: em\_gss\_pin.\*
- 21: em\_gss\_vrt.\*
- 22: em\_gss\_fun.\*
- 23: em\_gss\_mam.\*
- 24: em\_gss\_mus.\*
- 25: em\_gss\_other.\*
- 26: em\_gss\_pro.\*
- 27: em\_gss\_rtd.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	2.6	46	14 N78054	N78054 yv71g05.r1
2	28	1.6	28	14 R38968	R38968 yd07c08.s1
3	23.2	1.3	48	10 AW247978	AW247978 2839657.5
4	21.4	1.2	50	9 AU107934	AU107934 AU107934
5	21.2	1.2	36	17 AZ346286	AZ346286 LM0081C01
6	21	1.2	50	9 AU102877	AU102877 AU102877

C	7	21	1.2	50	9	AU105237
C	8	21	1.2	50	13	BM397711
C	9	20.8	1.2	46	17	AZ939393
C	10	20.6	1.2	48	17	AZ311362
C	11	20.6	1.2	50	9	AU106960
C	12	20.4	1.2	47	17	AZ313356
C	13	20.2	1.2	45	17	AZ985975
C	14	20.2	1.2	49	9	AA204601
C	15	20	1.1	40	9	A1475974
C	16	20	1.1	50	17	BH811451
C	17	19.8	1.1	40	14	W39000
C	18	19.4	1.1	50	9	AU104829
C	19	19.2	1.1	44	12	BG422154
C	20	19.2	1.1	49	17	AZ450961
C	21	19.2	1.1	50	9	AU103357
C	22	19.2	1.1	50	9	AU103358
C	23	19.2	1.1	50	9	AU103359
C	24	19.2	1.1	50	9	AU103361
C	25	19.2	1.1	50	9	AU103381
C	26	19.2	1.1	50	9	AU103915
C	27	19.2	1.1	50	9	AU106349
C	28	19.2	1.1	50	14	T74703
C	29	19	1.1	43	9	A1591257
C	30	19	1.1	49	17	AZ423762
C	31	19	1.1	50	9	AU107320
C	32	18.8	1.1	34	9	AA972479
C	33	18.8	1.1	43	17	BH857724
C	34	18.8	1.1	46	17	BH790015
C	35	18.8	1.1	50	9	AU102939
C	36	18.8	1.1	50	9	AU103583
C	37	18.8	1.1	50	9	AU104587
C	38	18.8	1.1	50	9	AU105918
C	39	18.6	1.1	44	17	TA165050
C	40	18.6	1.1	45	9	A1250043
C	41	18.6	1.1	49	17	AZ966392
C	42	18.6	1.1	50	9	AU103382
C	43	18.6	1.1	50	9	AU103553
C	44	18.6	1.1	50	9	AU104162
C	45	18.6	1.1	50	13	BI910989

ALIGNMENTS

RESULT 1  
N78054  
LOCUS  
DEFINITION  
N78054 46 bp mRNA linear EST 28-JAN-1997  
IMAGE:248216.5, similar to gb:X66363 SERINE/THREONINE-PROTEIN  
KINASE PCTAIRE-1 (HUMAN); mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
N78054.1 GI:1240755  
human.

REFERENCE

AUTHORS

REFERENCES

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

97044478

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

AU105237 AU105237  
BM397711 5009-0-35  
AZ939393 2M0279F13  
AZ311362 LM0026F16  
AU106960 AU106960  
AZ313356 LM0035H04  
AZ985975 2M0268F01  
AA204601 nu25C05.F  
A1475974 L196B06.X  
BH811451 SALK\_0586  
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AU104829 AU104829  
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AZ423762 LM0203E22  
AU107320 AU107320  
AA972479 OP42C10.S  
BH857724 SALK\_0159  
BH790015 SALK\_0529  
AU102939 AU102939  
AU103583 AU103583  
AU104587 AU104587  
AU105918 AU105918  
AL473116 T. brucei  
AT250043 ex48F02.X  
AZ966392 2M0236820  
AU103382 AU103382  
AU103553 AU103553  
AU104162 AU104162  
BI910989 603069394







**ORCANTISM**  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
**REFERENCE**  
**AUTHORS**  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly  
 , N., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,  
 and Wright, D., Weiss, R.  
**TITLE**  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
**JOURNAL**  
 Unpublished (2000)  
**COMMENT**  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SUIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0026 row: F column: 16  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 48.  
 Location/Qualifiers  
 1  
 48  
**FEATURES**  
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0026F16"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-."
/notes="Vector: PMD42sv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1473214/gb1AR29072.1), a copy-number inducible derivative of plasmid M1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
18 a 9 6 5 15

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BASE COUNT	18 a	9 c	6 g	15 t
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Best Local Similarity		67.4%	Pred. No. 7.8e+05;	
Matches	29;	Conservative	0;	Mismatches 14; Indels 0;

**OY** 1499 CTACTTCATATTGGCACTAAAGGAGATTACGCTACAAGA 1541  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
**DB** 5 CTAAATGCATCTTTTCTACTCAACTACAATCACCATTAAAGA 47

RESULT 11	50 bp	linear	EST 30-AUG-2001
AU106960/c	mrna		
LOCUS			
DEFINITION	Sugano Homo sapiens cDNA library	Homo sapiens	cDNA clone
ACCESSION	AU106960		
VERSION	CAS096689		mrna sequence.
KEYWORDS	AU106960		
EST.	AU106960.1	GI:13556481	
SOURCE	human		

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki.Y., Taira.H., Tsunoda.T., Mizushima-Sugano.J., Sese.J., Hata
H., Oka.T., Isogai.T., Tanaka.F., Morishita.S., Okubo.K., Sakaki
A., Nakamura.Y., Suyama.A. and Sugano.S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
COMMENT Contact: Yutaka Suzuki
Department of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ms.u-tokyo.ac.jp
Suzuki.Y., toshimoto@nakagawa.k., Maruyama.K., Suyama.A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
/clone_lib="Sugano Homo sapiens cDNA library"
/notes="Differential display comparison of untreated and
dimethylformate treated U937 cells"
BASE COUNT 7 a 14 c 18 g 11 t
ORIGIN
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Best Local Similarity 74.3%; Pred. NO. 7.9e+05;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 922 CTGTTCCAGCTCGCTGGCGTGGCTACTGCCA 956
DB 43 CTTTCCAGCTCGCTGGCGTGGCGTGGCGCAA 9
RESULT 12
A2331536/c
LOCUS 47 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0059H04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0059H04 R, DNA sequence.
ACCESSION A2331536
VERSION A2331536.1 GI:10394326
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 47)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLU, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0059 row: H column: 04
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 47.
Location/Qualifiers

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/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT 5 a 12 c 20 g 10 t
ORIGIN
Query Match 1.2%; Score 20.4; DB 17; Length 47;
Best Local Similarity 71.1%; Pred. NO. 8.6e+05;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 1644 GCTGCGAGGATGCCACACCCCTCACAGGCGGCCCA 1681
DB 38 GTTTCAGGCGGCGGCCCTCACAGGCGGCCCA 1
RESULT 13
A2985975
LOCUS 45 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0268F01F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0268F01 F, DNA sequence.
ACCESSION A2985975
VERSION A2985975.1 GI:13857202
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 45)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLU, UT
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Tel: 801 585 5606
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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0268 row: F column: 01
Seq primer: CTTGTAAAGCAGGCGCCAGT
Class: plasmid ends
High quality sequence stop: 45.
Location/Qualifiers

```



1. .45

/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGGC2M0268F01"  
/clone.lib="Mouse 10kb plasmid UGC2M library"  
/sex="female"  
/lab\_host="E. coli strain XL10-Gold, Tl-resistant, F-"  
/note="Vector: PWD2nrv; Purified genomic DNA from the Jackson  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD2 (gll147321419bIAFI29072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

18 a 0 c 24 g 3 t

BASE COUNT  
ORIGIN

```

High quality sequence stop: 1.
FEATURES
  Location/Qualifiers
    1..49
      /organism="Mus musculus"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone_lib="IMAGE:640424"
      /clone_lib="Soares_thymus_2NDMT"
      /sex="male"
      /tissue_type="Thymus"
      /dev_stage="4 weeks"
      /lab_host="DH10B"
      /note="vector: pTTT3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTCACATCATGATCGGAGCGCGGCTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector RNA
provided by Dr Bertrand Jordan. Library went through two
rounds of normalisation, and was constructed by Bento
Soares and M.Fatima Ronaldo."
    14 a 23 c 5 g 7 t
BASE COUNT
ORIGIN
Query Match          1.2%  Score 20.2:  DB 9;  Length 49;
Best Local Similarity 75.8%  Pred. No. 9.9e+05;
Matches 25;  Conservative 0;  Mismatches 8;  Indels 0;  Gaps 0.

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FEATURES
source
high quality sequence stop: 1.
Location/Qualifiers
1..40
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2134899"
/clone_lib="NCI_CGAP_Coll4"

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/tissue-type="moderately-differentiated adenocarcinoma"  
 /lab-host="DH10B"  
 /note="Organ: colon; Vector: PCWV-SPOFF6; Site\_1: SalI;  
 Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dr.  
 Average insert size 1.7 kb. Life Technologies catalog #:  
 11531-019"

BASE COUNT 9 a 13 c 14 g 4 t  
 ORIGIN

Query Match 1.1%; Score 20; DB 9; Length 40;  
 Best Local Similarity 72.2%; Pred. No. 1e+06;  
 Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
 QY 232 GGTGGTGGTGGCGGCGTGGACCTGGAGAGGCCCCC 267  
 ||||||||| | | ||||| || |||||  
 Db 39 GGTGGTGGTGTCTTTACCAACCTGGTGGACCCCCC 4

Search completed: March 4, 2003, 00:50:32  
 Job time : 2635 secs